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Asn Ser Asn Val Asp Pro Val Ser Leu Gly Leu Pro Gly Ala Leu Pro 50 55 60

Val Val Asn Ala Lys Gly Val Glu Trp Ala Ile Lys Ile Gly Leu Ala 65 70 75 80

Leu Asn Cys Ser Ile Ala Glu Ser Ser Arg Phe Ala Arg Lys Asn Tyr 85 90 95

Phe Tyr Pro Asp Gln Pro Lys Asn Tyr Gln Ile Ser Gln Tyr Asp Glu 100 105 110

Pro Ile Ala Tyr Asp Gly Tyr Leu Asp Val Val Leu Glu Asp Gly Thr 115 120 125

Glu Trp Arg Val Glu Ile Glu Arg Ala His Met Glu Glu Asp Thr Gly 130 135 140

Lys Leu Thr His Leu Gly Gly Thr Ser Gly Arg Ile His Gly Ala Thr 145 150 155 160

Ala Ser Leu Val Asp Cys Asn Arg Ala Gly Val Pro Leu Ile Glu Val 165 170 175

Val Thr Lys Pro Ile Glu Gly Ala Gly Ala Arg Ala Pro Glu Ile Ala 180 185 190

Lys Ala Tyr Val Ser Ala Leu Arg Asp Leu Val Lys Ala Leu Gly Val 195 200 205

Ser Asp Gly Arg Leu Asp Gln Gly Ser Met Arg Val Asp Ala Asn Leu 210 215 220

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Leu Ser Asp Ala Glu Met Arg Asp Leu Ile Asn Ala Asn Ala Leu Asp 50 60

Leu Ile Ile Glu Thr Val Glu Ala Gly Thr Thr Pro Asp Glu Ala Arg
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Ala Trp Trp Val Ser Tyr Ile Ser Gln Lys Ala Asn Glu Ser Gly Val 85 90 95

Glu Leu Asp Ala Leu Gly Val Ala Pro Ala His Val Ala Arg Val Val 100 105 110

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Ile Asp Gly Val Ile Ala Gly Glu Gly Asp Val Asp Ala Val Val Ala 130 135 140

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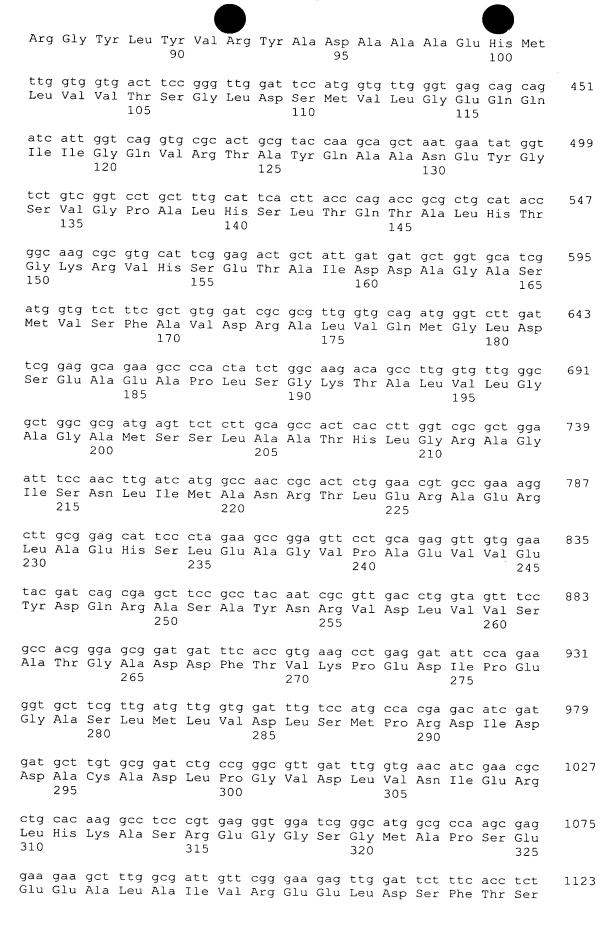
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330 335 gag cag cgc att cgc gat atc gtt cca gct gtg tcc gcg ttg cgc agg 1171 Glu Gln Arg Ile Arg Asp Ile Val Pro Ala Val Ser Ala Leu Arg Arg 345 350 cag gcc gcg tcg gtg gga agc gat gaa ttg gat cga ctc cgc caa cgt 1219 Gln Ala Ala Ser Val Gly Ser Asp Glu Leu Asp Arg Leu Arg Gln Arg 360 gcc ccc ggg att tcc gag gtg gaa tgg ggg gaa gtg gag aaa aca ggg 1267 Ala Pro Gly Ile Ser Glu Val Glu Trp Gly Glu Val Glu Lys Thr Gly 375 aga egg gte gte gat aag ett ett eat gaa eee aet gtg ege gte aag Arg Arg Val Val Asp Lys Leu Leu His Glu Pro Thr Val Arg Val Lys 390 395 gaa ctg gcg gcc cgg tcc ggc agc atc tct tat gat tca gct ctg caa 1363 Glu Leu Ala Ala Arg Ser Gly Ser Ile Ser Tyr Asp Ser Ala Leu Gln 410 gag ctg ttc ggt ttg gag tcg ctg gcg agc acc gca gca ccg gca acc 1411 Glu Leu Phe Gly Leu Glu Ser Leu Ala Ser Thr Ala Ala Pro Ala Thr 425 acg tcc gtc aac gcg tca gaa ctg ccg gat gcg ggt atc gtc gca ttc 1459 Thr Ser Val Asn Ala Ser Glu Leu Pro Asp Ala Gly Ile Val Ala Phe 440 gtg aac gca cct tct gcc aca caa acg agg gag taacatgacc ttaaaaattg 1512 Val Asn Ala Pro Ser Ala Thr Gln Thr Arg Glu 1515 gta <210> 386 <211> 464 <212> PRT <213> Corynebacterium glutamicum <400> 386 Met Val Ser Val Leu Ile Val Gly Met Ser His Arg Ser Ala Pro Val Ser Leu Leu Glu Arg Leu Ser Met Asp Asp Ser Val Arg Gly Glu Thr Thr Gln Ala Leu Leu Gly Arg Ala Ser Leu Ser Glu Ala Leu Ile Val Ser Thr Cys Asn Arg Leu Glu Val Tyr Thr Val Thr Ser Ser Phe His Thr Gly Val Asn Asp Val Val Glu Val Leu His Glu Ala Ser Gly Val 7.0 Asp Ile Glu Thr Leu Arg Gly Tyr Leu Tyr Val Arg Tyr Ala Asp Ala 90

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gat ggc gac gag ctg att gtg gga act ggc caa tac ggt ggt tcc cga 307 Asp Gly Asp Glu Leu Ile Val Gly Thr Gly Gln Tyr Gly Gly Ser Arg

atc tat cgc agc tcc gtt gat ggc cag gaa tct gtt tcc caa tcg ctt 355

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ccg Pro	atc Ile	ggc Gly	aag Lys 185	cac His	ggc Gly	ctg Leu	gct Ala	ctg Leu 190	att Ile	atc Ile	ggt Gly	cgc Arg	cct Pro 195	ggt Gly	ggc Gly	691
cct Pro	gat Asp	ttc Phe 200	Leu	gcc Ala	agc Ser	gaa Glu	gtg Val 205	gag Glu	cac His	tta Leu	ggc Gly	caa Gln 210	gtc Val	ggt Gly	gac Asp	739
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1 Ala		ı Lev				ı Leı	ı Gly				ı Alá	a Asr	n Ile 30	e Glr	ser	
Va]	L Asp				ı Arç	g Phe				y Th:	r Val		. Ası		o Leu	
Va:	l Ile	35 e Sei		e Pro	o Aro	g Ası	4(Vai		t Ala	a Ası	p Thi	4! r Ile		e Th:	r Ala	

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	gtg Val															451
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	gcg Ala 135															547
	gaa Glu															595
	gat Asp															643
	gaa Glu															691
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	gtg Val 215															787
	gga Gly															835
	atg Met															883
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Val Glu Leu Thr Val Ala Gly Arg Thr Asp Ala Gly Val His Ala Ala 50 55 60

Gly Gln Val Ala His Phe Asp Ile Pro Ala His Ala Leu Glu Gln Arg 65 70 75 80

Ser Ile Asp Gly Asp Pro Ser Lys Leu Val Arg Arg Leu Gly Arg Leu
85 90 95

Leu Pro Asp Asp Ile Arg Val His Gly Val Arg Phe Ala Glu Pro Gly 100 105 110

Phe Asp Ala Arg Phe Ser Ala Met Arg Arg His Tyr Val Tyr Arg Ile 115 120 125

Thr Thr His Pro Ala Gly Ala Leu Pro Thr Arg Arg His Asp Thr Ala 130 135 140

Gln Trp Pro Lys Pro Val Glu Leu Glu Arg Met Gln Leu Ala Ala Asp 145 150 155 160

Ala Leu Leu Gly Leu His Asp Phe Val Ala Phe Cys Lys Ala Lys Pro 165 170 175

His Ala Thr Thr Val Arg Glu Leu Gln Lys Phe Ala Trp Lys Asp Val 180 185 190

Ser Thr Asp Ile Glu Pro Gln Val Tyr Glu Ala His Val Val Ala Asp 195 200 205

Ala Phe Cys Trp Ser Met Val Arg Ser Leu Val Gly Ser Cys Met Ala 210 215 220

Val Gly Glu Gly Arg Arg Gly Ser Gly Phe Thr Ala Glu Leu Leu Asp 225 230 235 240

Ala Ser Glu Arg Ser Pro Met Val Pro Val Ala Pro Ala Lys Gly Leu 245 250 255

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gtg Val	gcg Ala	gca Ala	cat His 105	ccc Pro	acc Thr	gtg Val	ggt Gly	tgg Trp 110	gaa Glu	ggc	cca Pro	act Thr	gtg Val 115	gtg Val	ggc Gly	451
gga Gly	ctt Leu	gca Ala 120	gct Ala	gca Ala	ggt Gly	ttc Phe	cgc Arg 125	att Ile	tcc Ser	acc Thr	tcc Ser	ggc Gly 130	cca Pro	cca Pro	gag Glu	499

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Arg Lys Gly Ile Val Gln Arg Leu Asp Val Gly Thr Ser Gly Val Met

140

547

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Glu Lys Asp Ile Asn Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe 115 \blacksquare 120 125

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Asp Gln Thr Ile Asp Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys 180 185 190

Val Ile Pro Ser Arg Gly Ala Trp Leu Glu Phe Asp Val Asp Lys Arg 195 200 205

Asp Ser Val Gly Val Arg Ile Asp Arg Lys Arg Arg Gln Pro Val Thr 210 215 220

Val Leu Leu Lys Ala Leu Gly Trp Thr Thr Glu Gln Ile Thr Glu Arg 225 230 235 240

Phe Gly Phe Ser Glu Ile Met Met Ser Thr Leu Glu Ser Asp Gly Val

Ala Asn Thr Asp Glu Ala Leu Leu Glu Ile Tyr Arg Lys Gln Arg Pro 260 265 270

Gly Glu Gln Pro Thr Arg Asp Leu Ala Gln Ser Leu Leu Asp Asn Ser 275 280 285

Phe Phe Arg Ala Lys Arg Tyr Asp Leu Ala Arg Val Gly Arg Tyr Lys 290 295 300

Ile Asn Arg Lys Leu Gly Leu Gly Gly Asp His Asp Gly Leu Met Thr 305 310 315 320

Leu Thr Glu Glu Asp Ile Ala Thr Thr Ile Glu Tyr Leu Val Arg Leu 325 330 335

His Ala Gly Glu Arg Val Met Thr Ser Pro Asn Gly Glu Glu Ile Pro 340 345 350

Val Glu Thr Asp Asp Ile Asp His Phe Gly Asn Arg Arg Leu Arg Thr 355 360 365

Val Gly Glu Leu Ile Gln Asn Gln Val Arg Val Gly Leu Ser Arg Met 370 375 380

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Thr Pro Thr Ser Leu Ile Asn Val Arg Pro Val Ser Ala Ala Ile Arg
405 410 415

Glu Phe Phe Gly Thr Ser Gln Leu Ser Gln Phe Met Asp Gln Asn Asn

425

430

Ser Leu Ser Gly Leu Thr His Lys-Arg Arg Leu Ser Ala Leu Gly Pro 435 440 445

Gly Gly Leu Ser Arg Glu Arg Ala Gly Ile Glu Val Arg Asp Val His 450 455 460

Pro Ser His Tyr Gly Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro 465 470 475 480

Asn Ile Gly Leu Ile Gly Ser Leu Ala Ser Tyr Ala Arg Val Asn Pro 485 490 495

Phe Gly Phe Ile Glu Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu 500 505 510

Thr Asp Gln Ile Asp Tyr Leu Thr Ala Asp Glu Glu Asp Arg Phe Val 515 520 525

Val Ala Gln Ala Asn Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp 530 540

Glu Thr Val Thr Val Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly 545 550 555 560

Arg Asn Ala Val Asp Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser 565 570 575

Val Gly Thr Ala Met Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg 580 585 590

Ala Leu Met Gly Ala Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg 595 600 605

Ala Glu Ala Pro Phe Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr 610 620

Asp Ala Gly Asp Leu Val Ile Thr Pro Val Ala Gly Val Val Glu Asn 625 635 635

Val Ser Ala Asp Phe Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu 645 650 655

Thr Tyr Leu Leu Arg Lys Phe Gln Arg Thr Asn Gln Gly Thr Ser Tyr 660 665 670

Asn Gln Lys Pro Leu Val Asn Leu Gly Glu Arg Val Glu Ala Gly Gln 675 680 685

Val Ile Ala Asp Gly Pro Gly Thr Phe Asn Gly Glu Met Ser Leu Gly 690 695 700

Arg Asn Leu Leu Val Ala Phe Met Pro Trp Glu Gly His Asn Tyr Glu 705 710 715 720

Asp Ala Ile Ile Leu Asn Gln Asn Ile Val Glu Gln Asp Ile Leu Thr 725 730 735

Ser Ile His Ile Glu Glu His Glu Ile Asp Ala Arg Asp Thr Lys Leu 740 745 750

Gly Ala Glu Glu Ile Thr Arg Asp Ile Pro Asn Val Ser Glu Glu Val Leu Lys Asp Leu Asp Asp Arg Gly Ile Val Arg Ile Gly Ala Asp Val 770 Arg Asp Gly Asp Ile Leu Val Gly Lys Val Thr Pro Lys Gly Glu Thr Glu Leu Thr Pro Glu Glu Arg Leu Leu Arg Ala Ile Phe Gly Glu Lys 810 Ala Arg Glu Val Arg Asp Thr Ser Met Lys Val Pro His Gly Glu Thr 825 Gly Lys Val Ile Gly Val Arg His Phe Ser Arg Glu Asp Asp Asp 835 840 Leu <210> 397 <211> 469 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(469) <223> RXA01387 <400> 397 acgeegaeae egeatageag ateagaaaae aacegetaga aateaageea tacateeeee 60 ggacattgaa gagatgttet ggggggaaag ggagttttae gtg ete gae gta aac 115 Val Leu Asp Val Asn gto tto gat gag oto ogo ato ggo otg goo aco goo gao gao ato ogo 163 Val Phe Asp Glu Leu Arg Ile Gly Leu Ala Thr Ala Asp Asp Ile Arg 15 cgt tgg tcc aag ggt gag gtc aag aag ccg gag acc atc aac tac cga 211 Arg Trp Ser Lys Gly Glu Val Lys Lys Pro Glu Thr Ile Asn Tyr Arg acc ctc aag cct gag aag gac ggt ctg ttc tgc gag cgt atc ttc ggt 259 Thr Leu Lys Pro Glu Lys Asp Gly Leu Phe Cys Glu Arg Ile Phe Gly 40 45 cca act cgc gac tgg gag tgc gcc tgc ggt aag tac aag cgt gtc cgc 307 Pro Thr Arg Asp Trp Glu Cys Ala Cys Gly Lys Tyr Lys Arg Val Arg 55 tac aag ggc atc atc tgt gaa cgc tgt ggc gtt gag gtc acc aag tcc 355 Tyr Lys Gly Ile Ile Cys Glu Arg Cys Gly Val Glu Val Thr Lys Ser aag gtg cgc cgt gag cgc atg gga cac att gag ctc gct gca cca gta

403

Lys Val Arg Arg Glu Arg Met Gly His Ile Glu Leu Ala Ala Pro Val 90 95 100

acc cac att tgg tac ttc aag ggc gtt cca tca cgc ctc ggc tac ctt $\,$ 451 Thr His Ile Trp Tyr Phe Lys Gly Val Pro Ser Arg Leu Gly Tyr Leu $\,$ 105 $\,$ 110 $\,$ 115

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<212> PRT

<213> Corynebacterium glutamicum

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Thr Ile Asn Tyr Arg Thr Leu Lys Pro Glu Lys Asp Gly Leu Phe Cys 35 40 45

Glu Arg Ile Phe Gly Pro Thr Arg Asp Trp Glu Cys Ala Cys Gly Lys
50 55 60

Tyr Lys Arg Val Arg Tyr Lys Gly Ile Ile Cys Glu Arg Cys Gly Val 65 70 75 80

Glu Val Thr Lys Ser Lys Val Arg Arg Glu Arg Met Gly His Ile Glu 85 90 95

Leu Ala Ala Pro Val Thr His Ile Trp Tyr Phe Lys Gly Val Pro Ser 100 105 110

Arg Leu Gly Tyr Leu Leu Asp Leu Ala Pro Lys 115 120

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ctc tcc gca aac ggc act cca atg aag ctc gcg ggt gac gac gac gac 163

Leu Ser Ala Asn Gly Thr Pro Met Lys Leu Ala Gly Asp Asp Asp ttc gat cag gca ggc gcc tca att ggc atc aac ctg tcc cgt gac gag 211 Phe Asp Gln Ala Gly Ala Ser Ile Gly Ile Asn Leu Ser Arg Asp Glu cgt tee gae gee gae ace gea tageagatea gaaaacaace get 255 Arg Ser Asp Ala Asp Thr Ala 40 <210> 400 <211> 44 <212> PRT <213> Corynebacterium glutamicum <400> 400 Met Asn Glu Glu Val Leu Ser Ala Asn Gly Thr Pro Met Lys Leu Ala Gly Asp Asp Asp Phe Asp Gln Ala Gly Ala Ser Ile Gly Ile Asn Leu Ser Arg Asp Glu Arg Ser Asp Ala Asp Thr Ala <210> 401 <211> 1316 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(1293) <223> RXA01283 <400> 401 acc cgc cag ggt gtt cgc gtt cct gtc gct gct gag gtt ctg gat gca 48 Thr Arg Gln Gly Val Arg Val Pro Val Ala Ala Glu Val Leu Asp Ala act ggt gct gtc acc ggc tac acc cgc cat gac ctg atc gag act tct 96 Thr Gly Ala Val Thr Gly Tyr Thr Arg His Asp Leu Ile Glu Thr Ser gtc tcc ggt cgt gtt ctg gct ggc gat gca acc aac gct gca ggc gag 144 Val Ser Gly Arg Val Leu Ala Gly Asp Ala Thr Asn Ala Ala Gly Glu 35 gtt gtg ctt gct gct acc gac ctg acc gag ctc aac att gac ctt 192 Val Val Leu Ala Ala Gly Thr Asp Leu Thr Glu Leu Asn Ile Asp Leu 50 55 ctg gtc gag gct ggc atc aag gac gtc aag gtt cgt tcc gta ctt acc 240 Leu Val Glu Ala Gly Ile Lys Asp Val Lys Val Arg Ser Val Leu Thr tgc cag acc cca acc ggt gtt tgt gct aag tgc tac ggc aag tcc atg 288 Cys Gln Thr Pro Thr Gly Val Cys Ala Lys Cys Tyr Gly Lys Ser Met

85 90 gct tcc ggc cag cag gtt gat atc gga gag gct gtc ggt att gtt gct Ala Ser Gly Gln Gln Val Asp Ile Gly Glu Ala Val Gly Ile Val Ala 100 105 110 gca cag tcc att ggt gag cct ggt acc cag ctg acc atg cgt acc ttc 384 Ala Gln Ser Ile Gly Glu Pro Gly Thr Gln Leu Thr Met Arg Thr Phe 115 120 cac cag ggt ggt gtc ggt ggc gat att acc ggc ggt ctg cct cgt gtt 432 His Gln Gly Gly Val Gly Gly Asp Ile Thr Gly Gly Leu Pro Arg Val 130 135 140 cag gag ctg ttt gag gca cgt gtt cct aag aac tgt gca cca att gct Gln Glu Leu Phe Glu Ala Arg Val Pro Lys Asn Cys Ala Pro Ile Ala 145 150 155 tct gtt gaa ggt gtt atc cac ctt gag gat gaa ggc aac ttc tac act 528 Ser Val Glu Gly Val Ile His Leu Glu Asp Glu Gly Asn Phe Tyr Thr 165 ctg acc atc gtt cct gac gat ggc tcc gac aac gtt gtc tac gag aag 576 Leu Thr Ile Val Pro Asp Asp Gly Ser Asp Asn Val Val Tyr Glu Lys 180 ctg tcc aag cga cag ggt ctt gca tcc act cgc gtg gct atg gag tcc 624 Leu Ser Lys Arg Gln Gly Leu Ala Ser Thr Arg Val Ala Met Glu Ser 195 aac gct ggt gcg ttc att gag cgc acc ttg acc gaa ggt gac cgc gtc 672 Asn Ala Gly Ala Phe Ile Glu Arg Thr Leu Thr Glu Gly Asp Arg Val 210 acc gtt ggt cag cgt ctg ctc cgt ggt gca gct gat cca cac gac gtg 720 Thr Val Gly Gln Arg Leu Leu Arg Gly Ala Ala Asp Pro His Asp Val 225 230 ctc gag atc ctc ggt cgc cgc ggt gtg gag cag cac ctc atc tat gag 768 Leu Glu Ile Leu Gly Arg Arg Gly Val Glu Gln His Leu Ile Tyr Glu gtg cag gct gtt tac cgt gca cag ggt gtg gcc atc cac gac aag cac 816 Val Gln Ala Val Tyr Arg Ala Gln Gly Val Ala Ile His Asp Lys His 260 atc gaa atc atc att cgt cag atg ctg cgt cgc ggt acc gtc att gag 864 Ile Glu Ile Ile Arg Gln Met Leu Arg Arg Gly Thr Val Ile Glu 275 280 tee ggt tee ace gag tte ett eet ggt tet ttg gtt gae ete tet gag 912 Ser Gly Ser Thr Glu Phe Leu Pro Gly Ser Leu Val Asp Leu Ser Glu 290 295 gcg aag ctg gct aac tct gag gca atc ggt gcg ggc ggt cag cct gca Ala Lys Leu Ala Asn Ser Glu Ala Ile Gly Ala Gly Gly Gln Pro Ala 310 gag ctg cgt tct gag atc atg ggt atc acc aag qcc tct ctc qca act Glu Leu Arg Ser Glu Ile Met Gly Ile Thr Lys Ala Ser Leu Ala Thr 325 330

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ac Th	t ga r As	t gct p Ala 355	A A L S	ato Ile	aac Asn	aaq Lys	g cgc s Arg 360	Ser	gat Asp	aag Lys	ctc	atc Ile 365	ggc Gly	cto Leu	g aag 1 Lys	1104
gaq Gli	g aad 1 Asi 370	ı vaı	ato . Ile	: ato	ggt Gly	aag Lys 375	Leu	atc Ile	cca Pro	gct Ala	ggt Gly 380	act Thr	ggt Gly	att Ile	tcc Ser	1152
cgt Arc 385	9 T X T	c cgc Arg	aac Asn	atc Ile	tcc Ser 390	atc Ile	aag Lys	cca Pro	acc Thr	gag Glu 395	gct Ala	gct Ala	cgc Arg	aac Asn	gcc Ala 400	1200
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Thr 1 Thr Val	0> 4 Arg Gly Ser Val	O2 Gln Ala Gly 35	Gly Val 20 Arg	Val 5 Thr Val Ala	Arg Gly Leu Gly	Val Tyr Ala Thr 55	Pro Thr Gly 40 Asp	Val Arg 25 Asp Leu	10 His Ala Thr	Asp Thr Glu	Leu Asn Leu 60	Ile Ala 45 Asn	Glu 30 Ala Ile	15 Thr Gly Asp	Ser Glu Leu	
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Ser Val Glu Gly Val Ile His Leu Glu Asp Glu Gly Asn Phe Tyr Thr 165 170 175

Leu Thr Ile Val Pro Asp Asp Gly Ser Asp Asn Val Val Tyr Glu Lys 180 185

Leu Ser Lys Arg Gln Gly Leu Ala Ser Thr Arg Val Ala Met Glu Ser 195 200 205

Asn Ala Gly Ala Phe Ile Glu Arg Thr Leu Thr Glu Gly Asp Arg Val 210 215 220

Thr Val Gly Gln Arg Leu Leu Arg Gly Ala Ala Asp Pro His Asp Val 225 230 235 240

Leu Glu Ile Leu Gly Arg Arg Gly Val Glu Gln His Leu Ile Tyr Glu 245 250 255

Val Gln Ala Val Tyr Arg Ala Gln Gly Val Ala Ile His Asp Lys His 260 265 270

Ile Glu Ile Ile Ile Arg Gln Met Leu Arg Arg Gly Thr Val Ile Glu 275 280 285

Ser Gly Ser Thr Glu Phe Leu Pro Gly Ser Leu Val Asp Leu Ser Glu 290 295 300

Glu Leu Arg Ser Glu Ile Met Gly Ile Thr Lys Ala Ser Leu Ala Thr 325 330 335

Glu Ser Trp Leu Ser Ala Ala Ser Phe Gln Glu Thr Thr Arg Val Leu 340 345 350

Thr Asp Ala Ala Ile Asn Lys Arg Ser Asp Lys Leu Ile Gly Leu Lys 355 360 365

Glu Asn Val Ile Ile Gly Lys Leu Ile Pro Ala Gly Thr Gly Ile Ser 370 375 380

Arg Tyr Arg Asn Ile Ser Ile Lys Pro Thr Glu Ala Ala Arg Asn Ala 385 390 395 400

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<211> 201

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Arg His Glu Arg His Met Met Gln Ala Ala Arg Lys Tyr Gly Arg Lys 35 40 45

Pro Glu Asp Ala Gln Asp Ile Leu Gln Glu Ala Leu Phe Arg Ala Ser 50 55 60

Arg Asn Met His Leu Tyr Arg Ala Glu Ala Ala Leu Gly Thr Trp Leu 65 70 75 80

His Lys Leu Val Leu Asn Ser Gly Phe Asp Trp Ala Thr His Arg Ser 85 90 95

Gln Val Glu Phe Pro Ile Leu Asn Glu Pro Thr Ile Asp Leu Glu Lys 100 105 110

Asp Pro Arg Leu Ala Thr Asp Pro Leu Gly Tyr Leu Asp Val Ala Met 115 120 125

Thr Ile Arg Ser Ala Ile Asp Gln Leu His Pro Asp Gln Arg Ile Ala 130 135 140

Leu Ile Leu Val Asp Leu Gly Gly Tyr Thr Val Glu Asp Val Ala Glu

Ile Glu Gly Ile Lys Val Gly Thr Val Lys Ser Arg Arg Gly Arg Ala 165 170 175

Arg Lys Ala Leu Arg Ala Leu Leu His Ala Asp Phe Phe Gly Pro Glu 180 185 190

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							gcg Ala									163
-	-				-	_	ctc Leu			-						211
-			_	-		_	gat Asp 45				_					259
							ttc Phe									307
					_	_	aat Asn					_		_		355
	_		_		-		acc Thr		-	_				_		403
-		-	-			_	cat His					_	_		-	451
	_		_	_			ctg Leu 125		_				-			499
_				_	_	_	tac Tyr		_		_					547
_	_	_		_			gaa Glu		-			_	_	_		595
				_		_	ctc Leu		_		_		_		_	643
	-		_	_	_		aag Lys	_						_		691
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cgc																741

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Glu	atg Met 215	ctg Leu	ctt Leu	cgt Arg	cag Gln	tct Ser 220	cgc Arg	gat Asp	cca Pro	gtg Val	agc Ser 225	ttg Leu	gac Asp	atg Met	cca Pro	787
gtc Val 230																793

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Ala Glu Asp Glu Val Glu Leu Ala Gln Thr Ile Glu Val Gly Leu Tyr
Ala Glu His Leu Leu Lys Asn Ser Glu Glu Pro Leu Thr Arg Ala Met
Lys Arg Asp Leu Lys Val Leu Ala Lys Asp Gly Lys Lys Ala Arg Ser
His Leu Leu Glu Ala Asn Leu Arg Leu Val Val Ser Leu Ala Lys Arg
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Tyr Thr Gly Arg Gly Met Pro Leu Leu Asp Leu Ile Gln Glu Gly Asn
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Leu Gly Leu Ile Arg Ala Met Glu Lys Phe Asp Tyr Ser Lys Gly Phe
Lys Phe Ser Thr Tyr Ala Thr Trp Trp Ile Arg Gln Ala Ile Thr Arg
Gly Met Ala Asp Gln Ser Arg Thr Ile Arg Leu Pro Val His Leu Val
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Glu Gln Val Asn Lys Leu Ser Arg Ile Lys Arg Glu Leu Tyr Gln His
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cgc gag ctc gct gac ctg gta ccg cag gca acg gcg ggc gat cgt cgc Arg Glu Leu Ala Asp Leu Val Pro Gln Ala Thr Ala Gly Asp Arg Arg 10 15 20	
gca ttg caa aga ata atg gag att att cac ccc att gtt ttg cgt tat Ala Leu Gln Arg Ile Met Glu Ile Ile His Pro Ile Val Leu Arg Tyr 25 30 35	
gct cgc gct cgt att gga ggt gga cgc cag cca acg gca gaa gac gtt Ala Arg Ala Arg Ile Gly Gly Gly Arg Gln Pro Thr Ala Glu Asp Val 40 45 50	
gct caa gaa atc tgc ctg gcg gta gcc acc tcc att agg aac ttt gtc Ala Gln Glu Ile Cys Leu Ala Val Ala Thr Ser Ile Arg Asn Phe Val 55 60 65	
gac cag ggt agg ccg ttc atg gcg ttt gtc tac ggc att gca tct aac Asp Gln Gly Arg Pro Phe Met Ala Phe Val Tyr Gly Ile Ala Ser Asr 70 75 80 85	ı
aag gtc gca gat gct cac agg gcg atg tcg agg gat aaa tcg act cct Lys Val Ala Asp Ala His Arg Ala Met Ser Arg Asp Lys Ser Thr Pro 90 95 100	403
att gag gaa gtc cca gaa act tca cca gat act ttt acc ccc gaa gad Ile Glu Glu Val Pro Glu Thr Ser Pro Asp Thr Phe Thr Pro Glu Asp 105 110 115	
ttt gcg ctg gtc agc gat gga agt aac aga gtt agg gaa ctt ctc gat Phe Ala Leu Val Ser Asp Gly Ser Asn Arg Val Arg Glu Leu Leu Asp 120 125 130	
cta ctg agt gaa aag gca cgc gac att ctt atc ttg aga gtt atc gtt Leu Leu Ser Glu Lys Ala Arg Asp Ile Leu Ile Leu Arg Val Ile Val 135 140 145	
ggt ctt tcc gca gaa gaa act gca gag atg gtg ggc agc acc cca ggt Gly Leu Ser Ala Glu Glu Thr Ala Glu Met Val Gly Ser Thr Pro Gly 150 155 160	7
gct gta cga gtt gcc caa cac agg gca ctc acg aca ctt cga agc aca Ala Val Arg Val Ala Gln His Arg Ala Leu Thr Thr Leu Arg Ser Thr 170 175 180	
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<213> Corynebacterium glutamicum

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Ala Gly Asp Arg Ala Leu Gln Arg Ile Met Glu Ile Ile His Pro 20 25 30

Ile Val Leu Arg Tyr Ala Arg Ala Arg Ile Gly Gly Gly Arg Gln Pro $35 \hspace{1cm} 40 \hspace{1cm} 45$

Thr Ala Glu Asp Val Ala Gln Glu Ile Cys Leu Ala Val Ala Thr Ser 50 55 60

Ile Arg Asn Phe Val Asp Gln Gly Arg Pro Phe Met Ala Phe Val Tyr 65 70 75 80

Gly Ile Ala Ser Asn Lys Val Ala Asp Ala His Arg Ala Met Ser Arg 85 90 95

Asp Lys Ser Thr Pro Ile Glu Glu Val Pro Glu Thr Ser Pro Asp Thr $100 \hspace{1.5cm} 105 \hspace{1.5cm} 110 \hspace{1.5cm}$

Phe Thr Pro Glu Asp Phe Ala Leu Val Ser Asp Gly Ser Asn Arg Val 115 120 125

Arg Glu Leu Leu Asp Leu Leu Ser Glu Lys Ala Arg Asp Ile Leu Ile 130 135 140

Leu Arg Val Ile Val Gly Leu Ser Ala Glu Glu Thr Ala Glu Met Val 145 150 155 160

Gly Ser Thr Pro Gly Ala Val Arg Val Ala Gln His Arg Ala Leu Thr \$165\$ \$170\$ \$175\$

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cgg gaa acc caa gac gat gtc tgg cgt ctc ctc gcc cac ctt ggc ggc 144 Arg Glu Thr Gln Asp Asp Val Trp Arg Leu Leu Ala His Leu Gly Gly

35 45 cac gaa atc gcc gac gat cta acc caa gaa act tat ctg cgg gtc atg 192 His Glu Ile Ala Asp Asp Leu Thr Gln Glu Thr Tyr Leu Arg Val Met 55 age gee etc ecc ege tte gea geg ege tec teg geg ege acc tgg eta Ser Ala Leu Pro Arg Phe Ala Ala Arg Ser Ser Ala Arg Thr Trp Leu 75 cta tcg cta gcc cgg cgc gtc tgg gtc gac aac atc cga cac gac atg Leu Ser Leu Ala Arg Arg Val Trp Val Asp Asn Ile Arg His Asp Met 85 90 gca ege eee ege aaa tee ate gte gaa tae gaa gae ace ggt gee ace 336 Ala Arg Pro Arg Lys Ser Ile Val Glu Tyr Glu Asp Thr Gly Ala Thr 100 105 gac gcg agc aac gca ggc atc tgg tcc gag tgg atc gac gtg cgc acg 384 Asp Ala Ser Asn Ala Gly Ile Trp Ser Glu Trp Ile Asp Val Arg Thr 115 120 ctt atc gac gcc ctc cca ccc gaa cgc cgc gaa gcc ctc atc ctc acc 432 Leu Ile Asp Ala Leu Pro Pro Glu Arg Arg Glu Ala Leu Ile Leu Thr 130 caa gtg ttg ggc tac acc tac gaa gaa gcc gca aaa atc gcc gac gtc 480 Gln Val Leu Gly Tyr Thr Tyr Glu Glu Ala Ala Lys Ile Ala Asp Val 145 150 cga gtc gga aca atc cgt tcc cgc gta gcc cgc gcc aga gcg gac ctc 528 Arg Val Gly Thr Ile Arg Ser Arg Val Ala Arg Ala Arg Ala Asp Leu 165 170 att gct gca aca gct acc ggt gat tcc tca gcc gaa gat ggc aaa tcc 576 Ile Ala Ala Thr Ala Thr Gly Asp Ser Ser Ala Glu Asp Gly Lys Ser 180 gcc caa ggt tagcagatga gctacgtcaa cgg 608 Ala Gln Gly 195 <210> 412 <211> 195 <212> PRT <213> Corynebacterium glutamicum Ala Ile Val Lys Ser Lys Glu Arg Asn Asp Ala His Val Thr Glu Leu 15 Ala Leu Ala Ala Gly Arg Gly Asp Arg Ala Ala Leu Thr Asp Phe Ile 25 Arg Glu Thr Gln Asp Asp Val Trp Arg Leu Leu Ala His Leu Gly Gly 35 His Glu Ile Ala Asp Asp Leu Thr Gln Glu Thr Tyr Leu Arg Val Met

55

Ser Ala Leu Pro Arg Phe Ala Ala Arg Ser Ser Ala Arg Thr Trp Leu Leu Ser Leu Ala Arg Arg Val Trp Val Asp Asn Ile Arg His Asp Met Ala Arg Pro Arg Lys Ser Ile Val Glu Tyr Glu Asp Thr Gly Ala Thr Asp Ala Ser Asn Ala Gly Ile Trp Ser Glu Trp Ile Asp Val Arg Thr Leu Ile Asp Ala Leu Pro Pro Glu Arg Arg Glu Ala Leu Ile Leu Thr 135 Gln Val Leu Gly Tyr Thr Tyr Glu Glu Ala Ala Lys Ile Ala Asp Val 150 155 Arg Val Gly Thr Ile Arg Ser Arg Val Ala Arg Ala Arg Ala Asp Leu 170 Ile Ala Ala Thr Ala Thr Gly Asp Ser Ser Ala Glu Asp Gly Lys Ser 185 Ala Gln Gly 195 <210> 413 <211> 765 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(742) <223> RXA01530 <400> 413 cgcgccatcg ctcgtgacgg ccgcaaggcg aaaaaccacc tcctggaagc caaccttcgt 60 ctggttgtct ccctggcaaa gacgctacac cggccgtggc atg gca ttc ctg gac 115 Met Ala Phe Leu Asp ctc atc cag gaa ggc aac ctc ggt ctg att cgt gcc gta gag aag ttc 163 Leu Ile Gln Glu Gly Asn Leu Gly Leu Ile Arg Ala Val Glu Lys Phe 10 gac tac tcc aag ggc tac aag ttc tcc acc tac gca acc tgg tgg atc 211 Asp Tyr Ser Lys Gly Tyr Lys Phe Ser Thr Tyr Ala Thr Trp Trp Ile cgt cag gca atc acc cgc gcc atg gcc gac caa gca cga acc atc cgt 259 Arg Gln Ala Ile Thr Arg Ala Met Ala Asp Gln Ala Arg Thr Ile Arg 45 atc cca gtc cac atg gtt gaa gtg atc aac aaa ctt ggt cgc atc caa Ile Pro Val His Met Val Glu Val Ile Asn Lys Leu Gly Arg Ile Gln 5.5

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tac Tyr	gcc Ala	cgc Arg	gaa Glu 105	cca Pro	atc Ile	tcc Ser	ctg Leu	gac Asp 110	caa Gln	acc Thr	atc Ile	ggc Gly	gac Asp 115	gaa Glu	ggc Gly	451
gac Asp	agc Ser	cag Gln 120	ctc Leu	ggc Gly	gac Asp	ttc Phe	atc Ile 125	gaa Glu	gac Asp	tcc Ser	gaa Glu	gcc Ala 130	gtc Val	gtc Val	gca Ala	499
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tct Ser	aag Lys	ctg Leu 200	cgc Arg	cac His	cca Pro	tca Ser	cgc Arg 205	tcc Ser	cag Gln	gtc Val	ctt Leu	cgc Arg 210	gac Asp	tac Tyr	ctg Leu	739
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Ala Thr Trp Trp Ile Arg Gln Ala Ile Thr Arg Ala Met Ala Asp Gln

Ala Arg Thr Ile Arg Ile Pro Val His Met Val Glu Val Ile Asn Lys

Leu Gly Arg Ile Gln Arg Glu Leu Leu Gln Glu Leu Gly Arg Glu Pro

Thr Pro Gln Glu Leu Ser Lys Glu Met Asp Ile Ser Glu Glu Lys Val Leu Glu Ile Gln Gln Tyr Ala Arg Glu Pro Ile Ser Leu Asp Gln Thr 105 Ile Gly Asp Glu Gly Asp Ser Gln Leu Gly Asp Phe Ile Glu Asp Ser Glu Ala Val Val Ala Val Asp Ala Val Ser Phe Thr Leu Leu Gln Asp 135 Gln Leu Gln Asp Val Leu Glu Thr Leu Ser Glu Arg Glu Ala Gly Val 155 Val Lys Leu Arg Phe Gly Leu Thr Asp Gly Met Pro Arg Thr Leu Asp 165 170 Glu Ile Gly Gln Val Tyr Gly Val Thr Arg Glu Arg Ile Arg Gln Ile Glu Ser Lys Thr Met Ser Lys Leu Arg His Pro Ser Arg Ser Gln Val 200 Leu Arg Asp Tyr Leu Asp 210 <210> 415 <211> 1140 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1117) <223> RXA01531 <400> 415 taggeggaaa gggegttaag taettgeeat ttaateetea geateaeteg gateagtegg 60 agatgtcgat gaaaatgcac caggagccgt ggagagcagc atg gta gaa aac aac 115 Met Val Glu Asn Asn gta gca aaa aag acg gtc gct aaa aag acc gca cgc aag acc gca cgc Val Ala Lys Lys Thr Val Ala Lys Lys Thr Ala Arg Lys Thr Ala Arg 10 aaa gca gcc ccg cgc gtg gca acc cca ttg gga gtc gca tct gag tct 211 Lys Ala Ala Pro Arg Val Ala Thr Pro Leu Gly Val Ala Ser Glu Ser 25 ccc att tcg gcc acc cct gcg cgc agc atc gat gga acc tca acc cct Pro Ile Ser Ala Thr Pro Ala Arg Ser Ile Asp Gly Thr Ser Thr Pro 40 4.5 gtt gaa gct gct gac acc ata gag acc acc gcc cct gca gcg aag gct Val Glu Ala Ala Asp Thr Ile Glu Thr Thr Ala Pro Ala Ala Lys Ala 55 60





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cgg Arg	ccg Pro	tgg Trp 280	cat His	ggc Gly	att Ile	cct Pro	gga Gly 285	cct Pro	cat His	cca Pro	gga Gly	agg Arg 290	caa Gln	cct Pro	cgg Arg	979
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1117

1140

225

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Glu Met Glu Glu Ala Phe Ala Ala Gly Asp Lys Asp Ala Lys Leu Thr

230

220

Pro Ala Val Lys Arg Asp Leu Arg Ala Ile Ala Arg Asp Gly Arg Lys Ala Lys Asn His Leu Leu Glu Ala Asn Leu Arg Leu Val Val Ser Leu Ala Lys Thr Leu His Arg Pro Trp His Gly Ile Pro Gly Pro His Pro Gly Arg Gln Pro Arg Ser Asp Ser Cys Arg Arg Glu Val Arg Leu Leu 300 Gln Gly Leu Gln Val Leu His Leu Arg Asn Leu Val Asp Pro Ser Gly 315 320 Asn His Pro Arg His Gly Arg Pro Ser Thr Asn His Pro Tyr Pro Ser 330 Pro His Gly <210> 417 <211> 771 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(748) <223> RXA02065 <400> 417 cgagatgtga agtacctaca cgcattaagt gcaaatgaat tcacaattgc cagaagatgc 60 acaggatgta atctagattt cccaagttca gtggggcaaa atg act tat atg aaa Met Thr Tyr Met Lys 1 aag aag too oga gat gac goa ooo gto gta ato gaa aco gtt caa goa 163 Lys Lys Ser Arg Asp Asp Ala Pro Val Val Ile Glu Thr Val Gln Ala 15 gaa cat gct gaa gaa ctc acg ggc act gca gca ttc gat gct gga cag 211 Glu His Ala Glu Glu Leu Thr Gly Thr Ala Ala Phe Asp Ala Gly Gln 30 gca gac atg cca aca tgg ggc gag cta gtc gca gaa cat gca gat agc 259 Ala Asp Met Pro Thr Trp Gly Glu Leu Val Ala Glu His Ala Asp Ser 40 45 gtt tac cgc ctc gcg tac cgt ctt tcc ggc aac cag cac gat gct gaa 307 Val Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn Gln His Asp Ala Glu 55 60 gac ctg acc caa gaa aca ttc atg cgt gtc ttc cgc tcg ttg aag agc 355 Asp Leu Thr Gln Glu Thr Phe Met Arg Val Phe Arg Ser Leu Lys Ser 70 75 tac cag cca ggc acc ttt gag ggc tgg ctg cac cgc atc acc acc aac 403

BGI-127CP - 547 -

							,									
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Gln 65	His .	Asp	Ala	Glu	Asp 70	Leu	Thr	Gln	Glu	Thr 75	Phe	Met	Arg	Val	Phe 80	
Arg	Ser	Leu	Lys	Ser 85	Tyr	Gln	Pro	Gly	Thr 90	Phe	Glu	Gly	Trp	Leu 95	His	

105

Ile Arg Met Glu Ala Leu Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn 115 120 Asp Ile Thr Pro Glu Gln Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala 135 Leu Gln Ala Ala Leu Asp Glu Leu Ser Pro Asp Phe Arg Val Ala Val 155 Ile Leu Cys Asp Val Val Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr Leu Gly Val Lys Met Gly Thr Val Arg Ser Arg Ile His Arg Gly Arg 185 Ser Gln Leu Arg Ala Ser Leu Glu Ala Ala Ala Met Thr Ser Glu Glu 200 Val Ser Leu Leu Val Pro Thr His 210 <210> 419 <211> 645 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(622) <223> RXA00588 <400> 419 tcatacatct tggccccgga aaaccggggc caatcttatg gctcaagtcg ctagttagcc 60 gatgatccac ctctactgtt ccccaggagg gtaagtaatt atg gca agt gta gat 115 Met Ala Ser Val Asp aag caa tac atc acc cca gaa acc aag gcc aag ctg gag gaa gag ctc 163 Lys Gln Tyr Ile Thr Pro Glu Thr Lys Ala Lys Leu Glu Glu Glu Leu 10 aac gcc ctc atc gca cac cgc cct gca gtt gct gcg gaa atc aat gag 211 Asn Ala Leu Ile Ala His Arg Pro Ala Val Ala Ala Glu Ile Asn Glu cgc cgt gaa gaa ggc gac ctc aag gaa aac gct ggc tat gac gcc gct 259 Arg Arg Glu Glu Gly Asp Leu Lys Glu Asn Ala Gly Tyr Asp Ala Ala cgt gaa atg cag gac cag gaa gag gcc cgc atc aag cag atc tat gag 307 Arg Glu Met Gln Asp Gln Glu Glu Ala Arg Ile Lys Gln Ile Tyr Glu ctg ctg gcc aac tcc acc act gag cgc gaa ggc atc atc gaa ggt gtc 355 Leu Leu Ala Asn Ser Thr Thr Glu Arg Glu Gly Ile Ile Glu Gly Val 75 8.0

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aaa go Lys Al	ec geg .a Ala	aca Thr	ctc Leu 170	cgc Arg	ggc Gly	aaa Lys	aac Asn	taad	ccaaç	gga t	ittaa	aagt	c		642
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Ile Il									75					00	
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Asp Gl	y Asp	Glu 100	85 Asn	Ala Asp	Lys	Glu	Thr 105	90 Phe	Val Leu	Ile	Gly	Thr 110	95 Arg	Tyr Ala	
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Arg Ala Thr Gln Pro Ser Ala Pro Val Glu Gln Ala Gln Glu Ala Pro
1 5 10 15

gcg caa act tca act gca cct gct tca gca cca tct gaa gag act ccc 96 Ala Gln Thr Ser Thr Ala Pro Ala Ser Ala Pro Ser Glu Glu Thr Pro 20 25 30

gca gct ccc gct cgt gga cgt cgc cgt gta acc acc gcg acc $$ 144 Ala Ala Pro Ala Arg Arg Gly Arg Arg Arg Val Thr Thr Ala Thr $$ 35 $$ 40 $$ 45

acc cca gag cca gca gcg cct gca caa tcc cag cct gca gaa gct caa 192 Thr Pro Glu Pro Ala Ala Pro Ala Gln Ser Gln Pro Ala Glu Ala Gln 50 55 60

cca gca cag act cag gct gca cag caa gaa gaa ctt cct gtt gca gcg 240 Pro Ala Gln Thr Gln Ala Ala Gln Gln Glu Glu Leu Pro Val Ala Ala 65 70 75 80

aag gag too goa coa got aca gaa aac act cag ggo caa got cag ggo 288 Lys Glu Ser Ala Pro Ala Thr Glu Asn Thr Gln Gly Gln Ala Gln Gly 85 90

caa gct cag ggc caa gct cag ggc gat gag cac gat gat cgt ttt gag 336 Gln Ala Gln Gly Gln Ala Gln Gly Asp Glu His Asp Asp Arg Phe Glu 100 105

tcc cgt tct gct gca cgc cga gca cgc cgc aac cgt cag cgc cag atc 384
Ser Arg Ser Ala Ala Arg Arg Ala Arg Arg Asn Arg Gln Arg Gln Ile
115 120 125

cac cgc gat ggc gat gac aat gcg aat gca aac aca gag tct gag cag 432 His Arg Asp Gly Asp Asp Asn Ala Asn Ala Asn Thr Glu Ser Glu Gln 130 135 140

aac acc cct gcc cag aac gca acc gca cag gct gag tct gag cag act 480 Asn Thr Pro Ala Gln Asn Ala Thr Ala Gln Ala Glu Ser Glu Gln Thr 150 150 160

gca gct cct gca cag gct gaa gca gct gag cag aac cag aac gat aac 528
Ala Ala Pro Ala Gln Ala Glu Ala Ala Glu Gln Asn Gln Asn Asp Asn
165 170 175

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cgt Arg	tcc Ser	cgc Arg 195	ASI	aac Asn	cgg Arg	j aac j Asn	aat Asr 200	ı Arç	aat Asi	t tad n Tyi	c cgo r Arg	gat g Asp 205	Asr	c aa n Asi	c gag n Glu	624
tcc Ser	tct Ser 210	gat Asp	aat Asn	gca Ala	gga Gly	cag Gln 215	Ser	: agc : Ser	aat Asr	gat n Asp	gat Asp 220	Ala	gac Asp	aac Asi	c aat n Asn	672
cag Gln 225	gca Ala	cgg Arg	tct Ser	gag Glu	gac Asp 230	aat Asn	aac Asn	gac Asp	gat Asp	cgc Arg 235	, Arg	tct Ser	cgt Arg	aat Asr	aac Asn 240	720
cgt Arg	aac Asn	aac Asn	gac Asp	cgc Arg 245	aat Asn	gat Asp	cgt Arg	aac Asn	gat Asp 250	Arg	aat Asn	gac Asp	cgc Arg	gac Asp 255	aac Asn	768
АЗР	nsp	ASII	260	Asp	Arg	Arg	Asn	Arg 265	Arg	Gly	Arg	Arg	Asn 270	Arg	cgt Arg	816
gga Gly	9	275	АЗР	ALG	ASII	ASP	280	Asp	Asn	Arg	Asp	Asn 285	Arg	Asp	Asn	864
	290	ASII	ser	Asn	Asp	G1y 295	Asp	Asn	Asn	Gln	Gln 300	Asp	Glu	Leu	Gln	912
cag (Gln V 305	vai .	nia	сту	ite	310	Asp	11e	Val	Asp	His 315	Asn	Val	Ala	Phe	Val 320	960
cgc a Arg 1	1111	TIIT	СΙΫ	1yr 325	HIS	Ala	Ala	Pro	Ser 330	Asp	Val	Phe	Val	Ser 335	Asn	1008
cag c Gln I	Jeu .	ire i	340	Arg	Met	Gly	Leu	Arg 345	Ser	Gly	Asp	Ala	Ile 350	Glu	Gly	1056
cag g Gln V	(1	355	nec .	MSII I	2111	σтλ	360	СТÀ	Asn	His	Asn	Asn 365	His	Gly	Arg	1104
aac c Asn A 3	gt d rg (cag a Gln I	aag Lys '	tac a Tyr <i>i</i>	ASII .	aac Asn 375	ttg Leu	gtg Val	cgc Arg	gtg Val	gag Glu 380	atg Met	gtt Val	aac Asn	ggt Gly	1152
ctt c Leu P 385	ct g ro A	yct o	gaa (Glu (JLU .	hr 2 390	cgc (Arg <i>i</i>	aac Asn	cgt Arg	Pro	gag Glu 395	ttc Phe	ggc Gly	aag Lys	ctg Leu	act Thr 400	1200
cct c Pro L	tg t eu T	ac c 'yr F	10 F	aac d Asn (105	cag o	cgt (Arg 1	ctg (Leu <i>l</i>	Arg :	ttg Leu 410	gaa Glu	act Thr	gag (Glu (Gln	aag Lys 415	att Ile	1248
ctt a	cc a	ct c	gt ç	gtg a	tc q	gac t	tg a	atc a	atg	cct .	att (ggt a	aag	gga	cag	1296



Leu Thr Thr Arg Val Ile Asp Leu Ile Met Pro Ile Gly Lys Gly Gln 420 425 430

ctg tgc ttt gat tgt gtc gcc acc taaggctggt aagaccacga tcc Leu Cys Phe Asp Cys Val Ala Thr \$435\$

1343

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<211> 440

<212> PRT

<213> Corynebacterium glutamicum

<400> 422

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Ala Gl
n Thr Ser Thr Ala Pro Ala Ser Ala Pro Ser Glu Glu Thr Pro
 $20 \hspace{1cm} 25 \hspace{1cm} 30 \hspace{1cm}$

Ala Ala Pro Ala Arg Arg Gly Arg Arg Arg Val Thr Thr Ala Thr 35 40 45

Thr Pro Glu Pro Ala Ala Pro Ala Gln Ser Gln Pro Ala Glu Ala Gln 50 55 60

Pro Ala Gln Thr Gln Ala Ala Gln Glu Glu Leu Pro Val Ala Ala 65 70 75 80

Lys Glu Ser Ala Pro Ala Thr Glu Asn Thr Gln Gly Gln Ala Gln Gly 85 90 95

Gln Ala Gln Gly Gln Ala Gln Gly Asp Glu His Asp Asp Arg Phe Glu
100 105 110

Ser Arg Ser Ala Ala Arg Arg Ala Arg Arg Asn Arg Gln Arg Gln Ile 115 120 125

His Arg Asp Gly Asp Asp Asn Ala Asn Ala Asn Thr Glu Ser Glu Gln
130 135 140

Asn Thr Pro Ala Gln Asn Ala Thr Ala Gln Ala Glu Ser Glu Gln Thr 145 150 155 160

Ala Ala Pro Ala Gln Ala Glu Ala Ala Glu Gln Asn Gln Asn Asp Asn 165 170 175

Ser Glu Ser Ser Glu Asn Arg Ser Asp Asn Tyr Arg Asn Asn Asn Arg 180 185 190

Arg Ser Arg Asn Asn Arg Asn Arg Asn Tyr Arg Asp Asn Asn Glu

Ser Ser Asp Asn Ala Gly Gln Ser Ser Asn Asp Asp Ala Asp Asn Asn 210 215 220

Gln Ala Arg Ser Glu Asp Asn Asn Asp Asp Arg Arg Ser Arg Asn Asn 225 235 230 240

Arg Asn Asn Asp Arg Asn Asp Arg Asn Asp Arg Asn Asp Arg Asn Asp 245 250 255

Asp Asp Asn Asp Asp Arg Arg Asn Arg Arg Gly Arg Arg Asn Arg Arg 265 Gly Arg Asn Asp Arg Asn Asp Arg Asp Asn Arg Asp Asn Arg Asp Asn 280 Arg Asp Asn Ser Asn Asp Gly Asp Asn Asn Gln Gln Asp Glu Leu Gln 295 Gln Val Ala Gly Ile Leu Asp Ile Val Asp His Asn Val Ala Phe Val 310 Arg Thr Thr Gly Tyr His Ala Ala Pro Ser Asp Val Phe Val Ser Asn Gln Leu Ile Arg Arg Met Gly Leu Arg Ser Gly Asp Ala Ile Glu Gly Gln Val Arg Met Asn Gln Gly Gly Gly Asn His Asn Asn His Gly Arg Asn Arg Gln Lys Tyr Asn Asn Leu Val Arg Val Glu Met Val Asn Gly 375 Leu Pro Ala Glu Glu Thr Arg Asn Arg Pro Glu Phe Gly Lys Leu Thr 390 Pro Leu Tyr Pro Asn Gln Arg Leu Arg Leu Glu Thr Glu Gln Lys Ile 405 Leu Thr Thr Arg Val Ile Asp Leu Ile Met Pro Ile Gly Lys Gly Gln 420 430 Leu Cys Phe Asp Cys Val Ala Thr 435 <210> 423 <211> 960 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(937) <223> FRXA01723 <400> 423 cetteegeae eggttgagea ageacaagaa geteeegege aaaetteaae tgeaeetget 60 tcagcaccat ctgaagagac tcccgcagct cccgctcgtc gtg gac ktc agc cgt 115 Val Asp Xaa Ser Arg gta acc acc acc geg acc acc cca gag cca gca gcg cct gca caa tcc 163 Val Thr Thr Ala Thr Thr Pro Glu Pro Ala Ala Pro Ala Gln Ser 10 cag cct gca gaa gct caa cca gca cag act cag gct gca cag caa gaa Gln Pro Ala Glu Ala Gln Pro Ala Gln Thr Gln Ala Ala Gln Glu

25 30 gaa ett eet gtt gea geg aag gag tee gea eea get aca gaa aac act 259 Glu Leu Pro Val Ala Ala Lys Glu Ser Ala Pro Ala Thr Glu Asn Thr cag ggc caa kcy cag ggc caa gct cag ggc saa gct cag ggc gat gag 307 Gln Gly Gln Xaa Gln Gly Gln Ala Gln Gly Xaa Ala Gln Gly Asp Glu cac gat gat cgy ttt gag tcc cgt tct gct gca cgc cga gca cgc cgc 355 His Asp Asp Xaa Phe Glu Ser Arg Ser Ala Ala Arg Arg Ala Arg Arg aac cgt cag cgc cag atc cac cgc gat ggc gat gac aat gcg aat gca 403 Asn Arg Gln Arg Gln Ile His Arg Asp Gly Asp Asp Asn Ala Asn Ala 95 100 aac aca gag tet gag cag aac acc cet gee cag aac gea ace gea cag 451 Asn Thr Glu Ser Glu Gln Asn Thr Pro Ala Gln Asn Ala Thr Ala Gln 110 gct gag tct gag cag act gca gct cct gca cag gct gaa gca gct gag 499 Ala Glu Ser Glu Gln Thr Ala Ala Pro Ala Gln Ala Glu Ala Ala Glu 125 130 cag aac cag aac gat aac agc gag tcc tcc gag aac cgc agc gat aac 547 Gln Asn Gln Asn Asp Asn Ser Glu Ser Ser Glu Asn Arg Ser Asp Asn 135 140 tac cgc aac aac aat cgt cgt tcc cgc aac aac cgg aac aat cgc aat 595 Tyr Arg Asn Asn Asn Arg Arg Ser Arg Asn Asn Arg Asn Asn Arg Asn 150 155 tac cgc gat aac aac gag tcc tct gat aat gca gga cag tcc agc aat 643 Tyr Arg Asp Asn Asn Glu Ser Ser Asp Asn Ala Gly Gln Ser Ser Asn 170 175 gat gat gcc gac aac aat cag gca cgg tct gag gac aat aac gac gat 691 Asp Asp Ala Asp Asn Asn Gln Ala Arg Ser Glu Asp Asn Asn Asp Asp 185 cgc cgt tct cgt aat aac cgt aac aac gac cgc aat gat cgt aac gat 739 Arg Arg Ser Arg Asn Asn Arg Asn Asp Arg Asn Asp Arg Asn Asp 200 cgc aat gac cgc gac aac gac aac gat gat cgc cgc aac cgt cgc 787 Arg Asn Asp Arg Asp Asn Asp Asp Asp Asp Arg Arg Arg Arg 215 220 gga cgc cgc aat cgc cgt gga nen gca acg acc gta acg atc gcg aca 835 Gly Arg Arg Asn Arg Arg Gly Xaa Ala Thr Thr Val Thr Ile Ala Thr 230 acc gag ata acc ggg ata acc gcg aca aca gca acg atg gcg aca aca 883 Thr Glu Ile Thr Gly Ile Thr Ala Thr Thr Ala Thr Met Ala Thr Thr 250 acc agc aag atn gag nct gca gca ggt agc agg cat cct gga cat cgt 931 Thr Ser Lys Xaa Glu Xaa Ala Ala Gly Ser Arg His Pro Gly His Arg 270

gga cca taacgtcgca ttcgtgcgca cca Gly Pro

960

<210> 424

<211> 279

<212> PRT

<213> Corynebacterium glutamicum

<400> 424

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20 25 30

Ala Ala Gln Gln Glu Glu Leu Pro Val Ala Ala Lys Glu Ser Ala Pro 35 40 45

Ala Thr Glu Asn Thr Gln Gly Gln Xaa Gln Gly Gln Ala Gln Gly Xaa 50 55 60

Ala Gln Gly Asp Glu His Asp Asp Xaa Phe Glu Ser Arg Ser Ala Ala 65 70 75 80

Arg Arg Ala Arg Arg Asn Arg Gln Arg Gln Ile His Arg Asp Gly Asp 85 90 95

Asp Asn Ala Asn Ala Asn Thr Glu Ser Glu Gln Asn Thr Pro Ala Gln
100 105 110

Asn Ala Thr Ala Gln Ala Glu Ser Glu Gln Thr Ala Ala Pro Ala Gln 115 120 125

Ala Glu Ala Ala Glu Gln Asn Gln Asn Asp Asn Ser Glu Ser Ser Glu 130 135 140

Asn Arg Ser Asp Asn Tyr Arg Asn Asn Asn Arg Arg Ser Arg Asn Asn 145 150 155 160

Arg Asn Asn Arg Asn Tyr Arg Asp Asn Asn Glu Ser Ser Asp Asn Ala

Gly Gln Ser Ser Asn Asp Asp Ala Asp Asn Asn Gln Ala Arg Ser Glu 180 185 190

Asp Asn Asp Asp Arg Arg Ser Arg Asn Asn Arg Asn Asn Asp Arg 195 200 205

Asn Asp Arg Asn Asp Arg Asn Asp Arg Asp Asn Asp Asp Asn Asp Asp 210 215 220

Arg Arg Asn Arg Arg Gly Arg Arg Asn Arg Arg Gly Xaa Ala Thr Thr 225 230 235 240

Val Thr Ile Ala Thr Thr Glu Ile Thr Gly Ile Thr Ala Thr Thr Ala 245 250 255

Thr Met Ala Thr Thr Ser Lys Xaa Glu Xaa Ala Ala Gly Ser Arg

260 265 270

His Pro Gly His Arg Gly Pro 275

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<211> 507

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<213> Corynebacterium glutamicum

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aagatngagn ctgcagcagg tagcaggcat cctggacatc gtg gac cat aac gtc 115

Val Asp His Asn Val

gca ttc gtg cgc acc ggt tac cac gct gca cct tct gac gtg ttt $$ 163 Ala Phe Val Arg Thr Thr Gly Tyr His Ala Ala Pro Ser Asp Val Phe $$ 10 $$ 15 $$ 20

gtc agc aac cag ctg atc cgc cgt atg ggt ctt cgt tcc ggt gac gcc 211
Val Ser Asn Gln Leu Ile Arg Arg Met Gly Leu Arg Ser Gly Asp Ala
25 30

att gaa ggt cag gtt cgt atg aac cag ggt ggt ggc aac cac aac aac 259

Ile Glu Gly Gln Val Arg Met Asn Gln Gly Gly Gly Asn His Asn Asn
40
45
50

cat ggt cgc aac cgt cag aag tac aac aac ttg gtg cgc gtg gag atg 307 His Gly Arg Asn Arg Gln Lys Tyr Asn Asn Leu Val Arg Val Glu Met

gtt aac ggt ctt cct gct gaa gag act cgc aac cgt cct gag ttc ggc 355
Val Asn Gly Leu Pro Ala Glu Glu Thr Arg Asn Arg Pro Glu Phe Gly
70 80 85

aag ctg act cct ctg tac ccg aac cag cgt ctg cgt ttg gaa act gag 403 Lys Leu Thr Pro Leu Tyr Pro Asn Gln Arg Leu Arg Leu Glu Thr Glu 90 95 100

cag aag att ctt acc act cgt gtg atc gac ttg atc atg cct att ggt 451 Gln Lys Ile Leu Thr Thr Arg Val Ile Asp Leu Ile Met Pro Ile Gly 105 110 115

aag gga cag ctg tgc ttt gat tgt gtc gcc acc taaggctggt aagaccacga 504 Lys Gly Gln Leu Cys Phe Asp Cys Val Ala Thr 120 125

tcc 507

<210> 426 <211> 128

<212> PRT

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atcgacttga tcatgcctat tggtaaggga cagctgtgct ttg att gtg tcg cca 115 Leu Ile Val Ser Pro cct aag gct ggt aag acc acg atc ctg cag aac att gcg aac gct att 163 Pro Lys Ala Gly Lys Thr Thr Ile Leu Gln Asn Ile Ala Asn Ala Ile 10 15 tcc acc aac cca gag tgc tac ctc atg gtt gtt ttg gtt gat gag 211 Ser Thr Asn Asn Pro Glu Cys Tyr Leu Met Val Val Leu Val Asp Glu 25 30 cgt ccg aaa gaa gtt act gat atg cag cgc tcc gtc aac ggc gaa gtg 259 Arg Pro Lys Glu Val Thr Asp Met Gln Arg Ser Val Asn Gly Glu Val 40 45 att tot tot act tto gat ogt oca oca toa gag cao act gog gtt got



т.	- 1	0	~													
1	те	ser	Ser	Thr	Phe	Asp	Ara	Pro	Pro	Sar	C111	U.i.o	m L	7.1.		Ala
							9	LLO		261	GIU	$n \perp S$	III	Ата	vaı	Ala
		55					60					~ -				
							0.0					h h				

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330

<210> 428

<211> 69 <212> PRT

<213> Corynebacterium glutamicum

<400> 428

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Ile Ala Asn Ala Ile Ser Thr Asn Asn Pro Glu Cys Tyr Leu Met Val 20 25 30

Val Leu Val Asp Glu Arg Pro Lys Glu Val Thr Asp Met Gln Arg Ser

Val Asn Gly Glu Val Ile Ser Ser Thr Phe Asp Arg Pro Pro Ser Glu 50 55 60

His Thr Ala Val Ala 65

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Leu Val Asp Glu Arg

1

ccg aaa gaa gtt act gat atg cag cgc tcc gtc aac ggc gaa gtg att 163
Pro Lys Glu Val Thr Asp Met Gln Arg Ser Val Asn Gly Glu Val Ile

tct tct act ttc gat cgt cca cca tca gag cac act gcg gtt gct
Ser Ser Thr Phe Asp Arg Pro Pro Ser Glu His Thr Ala Val Ala
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tgagctggcg attgagcgtg cga 231

<210> 430

<211> 36

<212> PRT

<213> Corynebacterium glutamicum

<400> 430

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Asn Gly Glu Val Ile Ser Ser Thr Phe Asp Arg Pro Pro Ser Glu His 20 25 30

Thr Ala Val Ala 35

<210> 431

<211> 696

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(673)

<223> RXA01726

<400> 431

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- tcttctactt tcgatcgtcc accatcagag cacactgcgg ttg ctt gag ctg gcg 115 Leu Leu Glu Leu Ala 1 5
- att gag cgt gcg aag cgc ctg gtg gag cag ggc cag gac gtc gtt gtt 163

 Ile Glu Arg Ala Lys Arg Leu Val Glu Gln Gly Gln Asp Val Val

 10 15 20
- ctg ctt gac tcc att act cgt ttg ggc cgt gcg tac aac aac agc tca 211 Leu Leu Asp Ser Ile Thr Arg Leu Gly Arg Ala Tyr Asn Asn Ser Ser 25 30 35
- cct gca tcg gga cgt att ttg tcc ggt ggt gtg gat tcc aat gca ctg 259
 Pro Ala Ser Gly Arg Ile Leu Ser Gly Gly Val Asp Ser Asn Ala Leu
 40 45 50
- tac ccg ccg aag cgt ttc ttg ggt gct cga aac atc gaa aat ggt 307
 Tyr Pro Pro Lys Arg Phe Leu Gly Ala Ala Arg Asn Ile Glu Asn Gly
 55 60 65
- gga tot ttg acc atc atc gca act gcc atg gtg gaa acc ggc tot gct
 Gly Ser Leu Thr Ile Ile Ala Thr Ala Met Val Glu Thr Gly Ser Ala
 70 80 85
- ggt gac acc gtg atc ttc gag gag ttc aag ggc act ggt aac gct gag

 Gly Asp Thr Val Ile Phe Glu Glu Phe Lys Gly Thr Gly Asn Ala Glu

 90

 95

 100
- ctg aag ctg gat cgt aag atc tct gag cgc cgc gtt ttc cca gct gtg 451 Leu Lys Leu Asp Arg Lys Ile Ser Glu Arg Arg Val Phe Pro Ala Val 105 110 115
- gat gtt aat cct tct ggt act cgt aag gac gag ctg ttg ctc aac ccg Asp Val Asn Pro Ser Gly Thr Arg Lys Asp Glu Leu Leu Asn Pro 120 125 130
- gac gag gct cgc att atg cac aag ctg cgt cgt att ctg tct gca ctt 547

643

693

As	sp G 1	lu A 35	la A	rg I	le Me	et Hi 14	s L ₃	ys Le	eu Ar	cg Ai	ng Il 14	e Le	eu S∈	er Al	a Leu
ga As 15	-	at c sn G	ag c ln G	aa go ln Al	cc at la Il 15	e As	it ct p Le	ig tt eu Le	g at u Il	c aa e Ly 16	s Gl	g ct n Le	g aa u Ly	g aa s Ly	g acc s Thr 165
aa Ly	g to s Se	er A	at g sn A	cg ga la Gl 17	u FI	c ct e Le	c at u Me	g ca t Gl	g gt n Va 17	I Al	t tc a Se	c ag r Se	c gc r Al	t cc a Pr	a atg o Met O
gc Al	a go a Gl	jc ad .y Ti		aa aa lu Ly 35	a ga 's Gl	g ga u Gl	g ga u As	t ta p Ty 19	r Se	c ta r	atgg	catc	gca	ggtt	tct
gc	a														
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Gln	Asp	o Va	l Va 2	l Vai	l Leu	ı Leu	ı Asp	Ser 25	: Ile	e Thr	Arg	Leu	. Gly 30		Ala
Tyr	Asr	n As	n Se 5	r Sei	Pro	Ala	Ser 40	Gly	⁄ Arg	, Ile	: Leu	Ser 45	Gly	Gly	Val
Asp	Ser 50	As:	n Al	a Leu	ı Tyr	Pro 55	Pro	Lys	Arg	Phe	Leu 60	Gly	Ala	Ala	Arg
Asn 65	Ile	e Gli	ı Ası	n Gly	7 Gly	Ser	Leu	Thr	Ile	Ile 75	Ala	Thr	Ala	Met	Val 80
Glu	Thr	Gl	/ Sei	Ala 85	Gly	Asp	Thr	Val	Ile 90	Phe	Glu	Glu	Phe	Lys 95	Gly
Thr	Gly	Asr	100	a Glu	Leu	Lys	Leu	Asp 105	Arg	Lys	Ile	Ser	Glu 110	Arg	Arg
Val	Phe	Pro 115	Ala	val	Asp	Val	Asn 120	Pro	Ser	Gly	Thr	Arg 125	Lys	Asp	Glu
Leu	Leu 130	Leu	Asn	Pro	Asp	Glu 135	Ala	Arg	Ile	Met	His 140	Lys	Leu	Arg	Arg
Ile 145	Leu	Ser	Ala	Leu	Asp 150	Asn	Gln	Gln	Ala	Ile 155	Asp	Leu	Leu	Ile	Lys 160
Gln	Leu	Lys	Lys	Thr 165	Lys	Ser	Asn	Ala	Glu 170	Phe	Leu	Met	Gln	Val 175	Ala
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atq Met	g cco	g tto D Lei	g gto ı Val 20	L val	att L Il∈	aca Thr	a gaa Glu	acc Thr 25	Asp	cto Leu	g act 1 Thr	ggt Gly	aac Asr 30	Arg	gtt Val	96
ggc Gly	gat Asp	att O Ile 35	ATS	a GlŽ a dāč	g gcg ⁄ Ala	g aaa Lys	cgt Arg 40	Arg	cct Pro	gca Ala	ı aaa Lys	cgc Arg 45	Arg	aac Asn	aag Lys	144
gtg Val	gat Asp 50	, FIC	ttg Leu	geg Ala	r ctg Leu	gag Glu 55	Pro	Gly	gat Asp	ttg Leu	gtg Val 60	gtt Val	cat His	gaa Glu	acc Thr	192
cac His 65	GTA	att Ile	ggt Gly	cgt Arg	ttt Phe 70	gtg Val	aag Lys	atg Met	act Thr	gaa Glu 75	cga Arg	acc Thr	att Ile	tct Ser	gcg Ala 80	240
ggt Gly	gat Asp	gag Glu	acc Thr	tcg Ser 85	cgc Arg	cgt Arg	gaa Glu	tac Tyr	att Ile 90	gtg Val	ctg Leu	gag Glu	tac Tyr	gcg Ala 95	cca Pro	288
tct Ser	aag Lys	cgc Arg	gga Gly 100	cag Gln	ccc Pro	ggc Gly	gat Asp	cag Gln 105	ctg Leu	tat Tyr	gtg Val	ccg Pro	atg Met 110	gat Asp	gcg Ala	336
ctg Leu	gat Asp	atg Met 115	ctc Leu	agc Ser	cgc Arg	tac Tyr	gtc Val 120	ggt Gly	ggc Gly	gag Glu	aag Lys	ccg Pro 125	acg Thr	ctg Leu	tcc Ser	384
aaa Lys	atg Met 130	ggt Gly	ggt Gly	tct Ser	gac Asp	tgg Trp 135	aag Lys	aac Asn	gcc Ala	aag Lys	aag Lys 140	aag Lys	gct Ala	cgc Arg	gct Ala	432
gcc Ala 145	gtg Val	cgt Arg	gaa Glu	atc Ile	gcc Ala 150	ggt Gly	gag Glu	ctg Leu	gta Val	gaa Glu 155	ctc Leu	tac Tyr	gct Ala	aag Lys	cgc Arg 160	480
caa Gln	tcc Ser	gcg Ala	ccg Pro	ggt Gly 165	cac His	ccg Pro	ttt Phe	gcg Ala	ccg Pro 170	gat Asp	acg Thr	ccg Pro	tgg Trp	caa Gln 175	aaa Lys	528
gag Glu	atg Met	gaa Glu	gat Asp 180	aac Asn	ttc Phe	ccc Pro	tac Tyr	gtt Val 185	gag Glu	acc Thr	gaa Glu	gac Asp	cag Gln 190	atg Met	ttg Leu	576
gcg Ala	atc Ile	gat Asp	gcg Ala	gtc Val	aag Lys	gag Glu	gac Asp	atg Met	gag Glu	aaa Lys	agt Ser	gtc Val	ccc Pro	atg Met	gac Asp	624

195 200 205 cgc gtc atc atc ggc gat gtg ggt tat ggc aag acg gaa gtg gcg gtg 672 Arg Val Ile Ile Gly Asp Val Gly Tyr Gly Lys Thr Glu Val Ala Val 210 cgc gcg gcg ttc aag gct gtg caa gac ggc aag cag gta gcc gtt ctg 720 Arg Ala Ala Phe Lys Ala Val Gln Asp Gly Lys Gln Val Ala Val Leu gtg ccc acc acg ttg ctt gcg cag cag cac cag tcc acg ttt gaa gag 768 Val Pro Thr Thr Leu Leu Ala Gln Gln His Gln Ser Thr Phe Glu Glu 245 cgt atg act ggt ttc cct gtc acc atc aag gga ttg tca cgc ttt act 816 Arg Met Thr Gly Phe Pro Val Thr Ile Lys Gly Leu Ser Arg Phe Thr 260 265 270 tcg cct gcg gaa tcg cgg gag att ctc tcc ggt ttg gct gca gga tcg 864 Ser Pro Ala Glu Ser Arg Glu Ile Leu Ser Gly Leu Ala Ala Gly Ser 275 280 gtg gat atc gtc atc ggt act cac cgt ttg ctg cag act ggc gtg cag 912 Val Asp Ile Val Ile Gly Thr His Arg Leu Leu Gln Thr Gly Val Gln 290 295 tgg aaa aac cta ggg ctt gtc att gtg gat gag gag cag cgt ttc ggc 960 Trp Lys Asn Leu Gly Leu Val Ile Val Asp Glu Glu Gln Arg Phe Gly 315 gtg gaa cat aag gag cac atc aag gct ctg cgt act cac gtg gat gtg Val Glu His Lys Glu His Ile Lys Ala Leu Arg Thr His Val Asp Val 1008 325 335 ctg acc atg tcc gcg acc ccg att ccg cgc acc ctg gaa atg tcc atg 1056 Leu Thr Met Ser Ala Thr Pro Ile Pro Arg Thr Leu Glu Met Ser Met 340 gcc ggt atc cgt gag atg acc acc atg ctc acc ccg ccg gaa gat cgc 1104 Ala Gly Ile Arg Glu Met Thr Thr Met Leu Thr Pro Pro Glu Asp Arg 360 cac cca att ctt acc tat gtg gga ccg tat gaa gac aag cag gtc gcg 1152 His Pro Ile Leu Thr Tyr Val Gly Pro Tyr Glu Asp Lys Gln Val Ala 370 375 gca tca att cgc cgt gag ctg ctg cgc gat ggc cag gtc ttt ttc atc 1200 Ala Ser Ile Arg Arg Glu Leu Leu Arg Asp Gly Gln Val Phe Phe Ile 385 390 cac aac aag gtg gca gat att gag aag aag gcc cgc gag atc cgc gat His Asn Lys Val Ala Asp Ile Glu Lys Lys Ala Arg Glu Ile Arg Asp 1248 405 415 cta gtt ccc gaa gcc cga gtg gtc gtt gcc cac ggc cag atg agt gaa 1296 Leu Val Pro Glu Ala Arg Val Val Ala His Gly Gln Met Ser Glu 420 gag ctg ctg gaa caa acc gtt caa ggt ttc tgg gac cgc gaa tac gat Glu Leu Leu Glu Gln Thr Val Gln Gly Phe Trp Asp Arg Glu Tyr Asp 1344

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Val	Leu 450	Val	Cys	Thr	Thr	Ile 455	Val	Ğlu	Thr	Gly	Leu 460	Asp	Ile	Ser	Asn	
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	cac His					_			_		_		_			1488
	tac Tyr															1536
	cgc Arg															1584
	gtt Val 530															1632
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	cgc Arg															1728
	aaa Lys															1776
	ctt Leu								-	_				-		1824
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Met	Pro	Leu	Val 20	Val	Ile	Thr	Glu	Thr 25	Asp	Leu	Thr	Gly	Asn 30	Arg	Val	

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Leu Thr Met Ser Ala Thr Pro Ile Pro Arg Thr Leu Glu Met Ser Met

Ala Gly Ile Arg Glu Met Thr Thr Met Leu Thr Pro Pro Glu Asp Arg 355 360 365

His Pro Ile Leu Thr Tyr Val Gly Pro Tyr Glu Asp Lys Gln Val Ala 370 375 380

Ala Ser Ile Arg Arg Glu Leu Leu Arg Asp Gly Gln Val Phe Phe Ile 385 390 395 400

Leu Val Pro Glu Ala Arg Val Val Val Ala His Gly Gln Met Ser Glu 420 425 430

Glu Leu Leu Glu Gln Thr Val Gln Gly Phe Trp Asp Arg Glu Tyr Asp 435 440 445

Val Leu Val Cys Thr Thr Ile Val Glu Thr Gly Leu Asp Ile Ser Asn 450 455 460

Ala Asn Thr Leu Ile Val Glu Asn Ala His His Met Gly Leu Ser Gln 465 470 475 480

Leu His Gln Leu Arg Gly Arg Val Gly Arg Ser Arg Glu Arg Gly Tyr \$485\$ \$490\$ \$495

Ala Tyr Phe Leu Tyr Pro Lys Gly Ala Thr Leu Thr Glu Met Ser Tyr 500 510

Asp Arg Leu Ala Thr Ile Ala Gln Asn Asn Asp Leu Gly Ala Gly Met 515 520 525

Ala Val Ala Met Lys Asp Leu Glu Met Arg Gly Ala Gly Asn Val Leu 530 540

Gly Ala Glu Gln Ser Gly His Ile Ala Gly Val Gly Phe Asp Leu Tyr 545 550 550 560

Val Arg Leu Val Gly Glu Ala Val Glu Ala Tyr Arg Ala Leu Ala Asp 565 570 575

Gly Lys Val Val Asp Gly Thr Val Lys Gly Pro Lys Glu Ile Arg Val 580 585 590

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Arg Leu Arg Leu Glu Ile Tyr Arg Lys Leu Ala Gln Ser Glu Ser Glu 610 615 620

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atc aag agc att gag att ttc ccg gca cgg gaa ttg ctc att act gaa 211 Ile Lys Ser Ile Glu Ile Phe Pro Ala Arg Glu Leu Ile Thr Glu gaa gtg gca tcg cgt gcg gag tct ctt att tct aag cac ccg ggc aac 259 Glu Val Ala Ser Arg Ala Glu Ser Leu Ile Ser Lys His Pro Gly Asn ccg acg ctt gtg gag atg ctg tcg agg att gcg gat tcc caa gat gtt 307 Pro Thr Leu Val Glu Met Leu Ser Arg Ile Ala Asp Ser Gln Asp Val gat ggc atg gag gcg ttg att ccg gcg ctg acg gat acg ccg atg gtt 355 Asp Gly Met Glu Ala Leu Ile Pro Ala Leu Thr Asp Thr Pro Met Val ccg atg ctg gag ctc atg ccg gaa aac acc cat gtg ttg gtg att gct 403 Pro Met Leu Glu Leu Met Pro Glu Asn Thr His Val Leu Val Ile Ala ccg gag aag gtg cgc cga cgc att gcg gat ctg gaa gca acc gat gct 451 Pro Glu Lys Val Arg Arg Ile Ala Asp Leu Glu Ala Thr Asp Ala 110 gag ttt ttg atg gct ggt tgg gaa gca gct gcg atg ggt gct gat ggt 499 Glu Phe Leu Met Ala Gly Trp Glu Ala Ala Ala Met Gly Ala Asp Gly 125 130 cca gtg gct gcg gaa ggc ctg gac ttg gaa gct tct agc tat cgc agt 547 Pro Val Ala Ala Glu Gly Leu Asp Leu Glu Ala Ser Ser Tyr Arg Ser 140 tat gaa agt ttg gag gtt tct gcg tcg aaa agc gat gtg cgt tgg tgg 595 Tyr Glu Ser Leu Glu Val Ser Ala Ser Lys Ser Asp Val Arg Trp Trp 155 act ttc gcg ccg ccg ggc atg ttt gag gcc tcg gag gag gcg acg ctg 643 Thr Phe Ala Pro Pro Gly Met Phe Glu Ala Ser Glu Glu Ala Thr Leu 170 ccg ctt gat ttt gaa gcc ggg ccg gcg ccg ggt gag ctg ccg aag 691 Pro Leu Asp Phe Glu Ala Gly Pro Ala Pro Arg Gly Glu Leu Pro Lys 195 atc gat gcg atg gtg cag ctg ctt gcg cac aca acc ggc ggt ggg 739 Ile Asp Ala Met Met Ala Gln Leu Leu Ala His Thr Thr Gly Gly

115

200 205 210 cgg gct gcg ttt atc gcg ccg acc caa ggt gcg att aag cgc atg gtc 787 Arg Ala Ala Phe Ile Ala Pro Thr Gln Gly Ala Ile Lys Arg Met Val 220 gat cgt ttc gcg gaa aag ggc att ccc acc cat gtg gcg acc ccg ggt Ásp Arg Phe Ála Glu Lys Gly Ile Pro Thr His Val Ála Thr Pro Gly 240 tgg gag cca acg cct ggt caa gtg act ctt tat cat gcg ctg agc cat Trp Glu Pro Thr Pro Gly Gln Val Thr Leu Tyr His Ala Leu Ser His 250 255 gct ggc ctg gtg ttt ccg aag gtg cgt aaa cac cgc gat ggc gct gca Ala Gly Leu Val Phe Pro Lys Val Arg Lys His Arg Asp Gly Ala Ala 265 270 atg ccg ttg gtg gtt att aca gaa acc gat ctg act ggt aac cgt gtt Met Pro Leu Val Val Ile Thr Glu Thr Asp Leu Thr Gly Asn Arg Val 979 280 285 ggc gat att gca ggg cga aac gtc gac ctg caa aac gcc gca aca agg 1027 GÍy Ásp Ile Ála GÍy Arg Asn Val Ásp Leu Gln Asn Ála Ála Thr Arg 300 tgg atc ctt tgg cgc tgg agc cag ggg att tgg tgg ttc atg aaa ccc 1075 Trp Ile Leu Trp Arg Trp Ser Gln Gly Ile Trp Trp Phe Met Lys Pro 320 acg gca ttg gtc gtt ttg tgaagatgac tgaacgaacc att 1116 Thr Ala Leu Val Val Leu 330 <210> 436 <211> 331 <212> PRT <213> Corynebacterium glutamicum Met Lys Val Ser Asp Ile Arg Gln Phe Ser Val Ala Asp Gln Arg Thr Ile Pro Glu Ile Thr Ile Lys Ser Ile Glu Ile Phe Pro Ala Arg Glu 25 Leu Leu Ile Thr Glu Glu Val Ala Ser Arg Ala Glu Ser Leu Ile Ser Lys His Pro Gly Asn Pro Thr Leu Val Glu Met Leu Ser Arg Ile Ala

Lys His Pro Gly Asn Pro Thr Leu Val Glu Met Leu Ser Arg Ile Ala Asp Ser Gln Asp Val Asp Gly Met Glu Ala Leu Ile Pro Ala Leu Thr 80 Asp Thr Pro Met Val Pro Met Leu Glu Leu Met Pro Glu Asn Thr His 95 Val Leu Val Ile Ala Asp Leu 100 Arg Arg Arg Ile Ala Asp Leu 100 Asp Leu 100 Asp Leu 110 Asp Leu 110 Asp Leu 110 Asp Leu

Glu Ala Thr Asp Ala Glu Phe Leu Met Ala Gly Trp Glu Ala Ala 115 120 125

Met Gly Ala Asp Gly Pro Val Ala Ala Glu Gly Leu Asp Leu Glu Ala 130 135 140

Ser Ser Tyr Arg Ser Tyr Glu Ser Leu Glu Val Ser Ala Ser Lys Ser 145 150 155 160

Asp Val Arg Trp Trp Thr Phe Ala Pro Pro Gly Met Phe Glu Ala Ser 165 170 175

Glu Glu Ala Thr Leu Pro Leu Asp Phe Glu Ala Gly Pro Ala Pro Arg 180 185 190

Gly Glu Leu Pro Lys Ile Asp Ala Met Met Ala Gln Leu Leu Ala His 195 200 205

Thr Thr Gly Gly Gly Arg Ala Ala Phe Ile Ala Pro Thr Gln Gly Ala 210 215 220

Ile Lys Arg Met Val Asp Arg Phe Ala Glu Lys Gly Ile Pro Thr His 235 230 235

Val Ala Thr Pro Gly Trp Glu Pro Thr Pro Gly Gln Val Thr Leu Tyr 245 250 255

His Ala Leu Ser His Ala Gly Leu Val Phe Pro Lys Val Arg Lys His 260 265 270

Arg Asp Gly Ala Ala Met Pro Leu Val Val Ile Thr Glu Thr Asp Leu 275 280 285

Thr Gly Asn Arg Val Gly Asp Ile Ala Gly Arg Asn Val Asp Leu Gln 290 295 300

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<211> 480

<212> DNA

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<222> (1)..(480)

<223> FRXA00737

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20 25 30 acg ccg atg gtt ccg atg ctg gag ctc atg ccg gaa aac acc cat gtg Thr Pro Met Val Pro Met Leu Glu Leu Met Pro Glu Asn Thr His Val 40 ttg gtg att gct ccg gag aag gtg cgc cga cgc att gcg gat ctg gaa 192 Leu Val Ile Ala Pro Glu Lys Val Arg Arg Arg Ile Ala Asp Leu Glu 55 gca acc gat gct gag ttt ttg atg gct ggt tgg gaa gca gct gcg atg 240 Ala Thr Asp Ala Glu Phe Leu Met Ala Gly Trp Glu Ala Ala Met 70 ggt gct gat ggt cca gtg gct gcg gaa ggc ctg gac ttg gaa gct tct 288 Gly Ala Asp Gly Pro Val Ala Ala Glu Gly Leu Asp Leu Glu Ala Ser 8.5 agc tat cgc agt tat gaa agt ttg gag gtt tct gcg tcg aaa agc gat 336 Ser Tyr Arg Ser Tyr Glu Ser Leu Glu Val Ser Ala Ser Lys Ser Asp 100 105 gtg cgt tgg tgg act ttc gcg ccg ccg ggc atg ttt gag gcc tcg gag 384 Val Arg Trp Trp Thr Phe Ala Pro Pro Gly Met Phe Glu Ala Ser Glu 115 125 gag gcg acg ctg ccg ctt gat ttt gaa gcc ggg ccg gcg ccg cgc ggt 432 Glu Ala Thr Leu Pro Leu Asp Phe Glu Ala Gly Pro Ala Pro Arg Gly 130 135 gag ctg ccg aag atc gat gcg atg atg gcg cag ctg ctt gcg cac aca 480 Glu Leu Pro Lys Ile Asp Ala Met Met Ala Gln Leu Leu Ala His Thr 150 <210> 438 <211> 160 <212> PRT <213> Corynebacterium glutamicum <400> 438 His Pro Gly Asn Pro Thr Leu Val Glu Met Leu Ser Arg Ile Ala Asp Ser Gln Asp Val Asp Gly Met Glu Ala Leu Ile Pro Ala Leu Thr Asp Thr Pro Met Val Pro Met Leu Glu Leu Met Pro Glu Asn Thr His Val 35 Leu Val Ile Ala Pro Glu Lys Val Arg Arg Ile Ala Asp Leu Glu Ala Thr Asp Ala Glu Phe Leu Met Ala Gly Trp Glu Ala Ala Met 65 75 Gly Ala Asp Gly Pro Val Ala Ala Glu Gly Leu Asp Leu Glu Ala Ser

Ser Tyr Arg Ser Tyr Glu Ser Leu Glu Val Ser Ala Ser Lys Ser Asp

105

110

Val Arg Trp Trp Thr Phe Ala Pro Pro Gly Met Phe Glu Ala Ser Glu 115 120 125

Glu Ala Thr Leu Pro Leu Asp Phe Glu Ala Gly Pro Ala Pro Arg Gly 130 135 140

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10 15 20

tca ggc cac cta acc gaa act gcc caa aga tta ggc atc ccg cag ccc 211 Ser Gly His Leu Thr Glu Thr Ala Gln Arg Leu Gly Ile Pro Gln Pro 25 30 35

aca ctt tcc aga cga atc agc cga gtg gaa aaa cac gca ggc acc cca 259
Thr Leu Ser Arg Arg Ile Ser Arg Val Glu Lys His Ala Gly Thr Pro
40
45

ctt ttc gac cgc ggc cgc aaa ctc gtc ctc aac caa cga ggc cac
Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu Asn Gln Arg Gly His
55 60 65

gcc ttc ctc aac cac gcc agc gcc atc gtc gca gaa ttc aac tcc gcc 355 Ala Phe Leu Asn His Ala Ser Ala Ile Val Ala Glu Phe Asn Ser Ala 70 75 80 85

gca act gaa atc aaa cgc ctc atg gac cca gaa aaa ggc aca atc cga Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu Lys Gly Thr Ile Arg 90 95 100

ctg gac ttc atg cat tcc ttg ggc act tgg atg gtc ccc gaa ctt atc 451 Leu Asp Phe Met His Ser Leu Gly Thr Trp Met Val Pro Glu Leu Ile 105 110 115

cga aca ttc cgc gcc gaa cac ccc aac gta gaa ttc caa ctc cac caa 499 Arg Thr Phe Arg Ala Glu His Pro Asn Val Glu Phe Gln Leu His Gln

												-50	•			
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ctc Leu 150	gca Ala	tta Leu	gtt Val	ggc Gly	ecc Pro 155	aaa Lys	cct Pro	gcc Ala	gag Glu	gtt Val 160	Gly	acc Thr	tct Ser	tta Leu	ggg Gly 165	595
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Ile Ser Val Ala Gln Ser Gly His Leu Thr Glu Thr Ala Gln Arg Leu

Gly Ile Pro Gln Pro Thr Leu Ser Arg Arg Ile Ser Arg Val Glu Lys

His Ala Gly Thr Pro Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu 50

Asn Gln Arg Gly His Ala Phe Leu Asn His Ala Ser Ala Ile Val Ala

Glu Phe Asn Ser Ala Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu

Lys Gly Thr Ile Arg Leu Asp Phe Met His Ser Leu Gly Thr Trp Met 105

85

Val Pro Glu Leu Ile Arg Thr Phe Arg Ala Glu His Pro Asn Val Glu

Phe Gln Leu His Gln Ala Ala Ala Met Leu Leu Val Asp Arg Val Leu 135

Ala Asp Glu Thr Asp Leu Ala Leu Val Gly Pro Lys Pro Ala Glu Val 150

Gly Thr Ser Leu Gly Trp Ala Pro Leu Leu Arg Gln Arg Leu Ala Leu 170

Ala Val Pro Ala Asp His Arg Leu Ala Ser Phe Ser Gly Gln Gly Glu 180 185

Leu Pro Leu Ile Thr Ala Ala Glu Glu Pro Phe Val Ala Met Arg Ala 200

Gly Phe Gly Thr Arg Leu Leu Met Asp Ala Leu Ala Glu Glu Ala Gly 210 215

Phe Val Pro Asn Val Val Phe Glu Ser Met Glu Leu Thr Thr Val Ala 235

Gly Leu Val Ser Ala Gly Leu Gly Val Gly Val Val Pro Met Asp Asp

Pro Tyr Leu Ser Thr Val Gly Ile Val Gln Arg Pro Leu Ser Pro Pro 265

Ala Tyr Arg Glu 275

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<223> FRXA01872

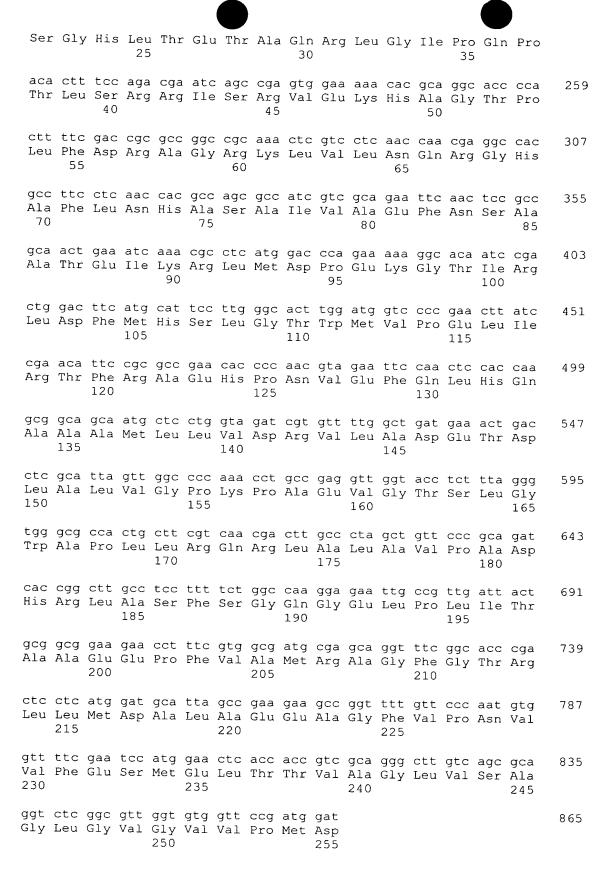
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gga gac ctg cga atc gac gac cta cgc agc ttc att tca gtc gct caa Gly Asp Leu Arg Ile Asp Asp Leu Arg Ser Phe Ile Ser Val Ala Gln

tca ggc cac cta acc gaa act gcc caa aga tta ggc atc ccg cag ccc



<211> 255

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<213> Corynebacterium glutamicum

<400> 442

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35 40 45

His Ala Gly Thr Pro Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu 50 55 60

Asn Gln Arg Gly His Ala Phe Leu Asn His Ala Ser Ala Ile Val Ala 65 70 75 80

Glu Phe Asn Ser Ala Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu 85 90 95

Val Pro Glu Leu Ile Arg Thr Phe Arg Ala Glu His Pro Asn Val Glu 115 120 125

Phe Gln Leu His Gln Ala Ala Met Leu Leu Val Asp Arg Val Leu 130 135 140

Ala Asp Glu Thr Asp Leu Ala Leu Val Gly Pro Lys Pro Ala Glu Val
145 150 155 160

Gly Thr Ser Leu Gly Trp Ala Pro Leu Leu Arg Gln Arg Leu Ala Leu 165 170 175

Ala Val Pro Ala Asp His Arg Leu Ala Ser Phe Ser Gly Gln Gly Glu 180 185 190

Leu Pro Leu Ile Thr Ala Ala Glu Glu Pro Phe Val Ala Met Arg Ala 195 200 205

Gly Phe Gly Thr Arg Leu Leu Met Asp Ala Leu Ala Glu Glu Ala Gly 210 215 220

Phe Val Pro Asn Val Val Phe Glu Ser Met Glu Leu Thr Thr Val Ala 225 230 235 240

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<210> 443

<211> 615

<212> DNA

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451

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615

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<213> Corynebacterium glutamicum

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155

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Gln Gln Asp Val Trp Leu Asp Val Trp Thr Met Arg Ile Gly Leu Pro 30 Ala Arg Leu Asp Ala Gln Leu Lys Glu Ala Ala Gly Val Ser His Phe Glu Tyr Phe Thr Met Ala Gln Ile Ser Met Ala Pro Glu His Arg Val Arg Met Ser Glu Leu Ala Glu Leu Ser Asp Met Thr Leu Ser His Leu Ser Arg Val Val Thr Arg Leu Glu Lys Ala Gly Trp Val Lys Arg Val Pro Asp Pro Asp Asp Gly Arg Ala Thr Val Ala Val Leu Thr Asp Ser Gly Trp Glu Lys Val Lys Ala Thr Ala Pro Gly His Val Lys Glu Val Arg Arg Leu Val Phe Asp Asp Leu Thr Pro Glu Glu Leu Lys Val Met 135 Gly Thr Ala Met Lys Lys Ile Val Asn Arg Leu Asp Met Ser Asn Arg Leu Pro Arg Val <210> 445 <211> 1022 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(999) <223> RXN01404 <400> 445 cag aag atg age aca tee ege eee aca att tat gae gte gee aaa gee 48 Gln Lys Met Ser Thr Ser Arg Pro Thr Ile Tyr Asp Val Ala Lys Ala -5 gca ggc gtc tcc aaa tcc ttg gtt tct ctc gtg ctt cgc ggc tcc ccc 96 Ala Gly Val Ser Lys Ser Leu Val Ser Leu Val Leu Arg Gly Ser Pro aac gtg agc aaa gaa tcc gaa gcc gcg gtc aag acc gcg ata aaa aag Asn Val Ser Lys Glu Ser Glu Ala Ala Val Lys Thr Ala Ile Lys Lys 144 ctc aac tac cag cca aat cgc gcc gca tca gac ctt gcg gcc aag cgc 192 Leu Asn Tyr Gln Pro Asn Arg Ala Ala Ser Asp Leu Ala Ala Lys Arg acg cag ctc att gca gtg ctt atc gac gac tac tcc aac ccg tgg ttc Thr Gln Leu Ile Ala Val Leu Ile Asp Asp Tyr Ser Asn Pro Trp Phe

65		70		75	80
atc gac	ctg att caa Leu Ile Gln 85	Ser Leu Se	c gat gtg r Asp Val 90	ctc acc ccc Leu Thr Pro	aag ggg tac 288 Lys Gly Tyr 95
cga ctg f Arg Leu S	tcc gtc att Ser Val Ile 100	gac tca tta Asp Ser Lei	a acc tct u Thr Ser 105	caa gcc ggc Gln Ala Gly	acc gat ccc 336 Thr Asp Pro 110
TIC III	agt gca cta Ser Ala Leu 115	tca atg cgc Ser Met Arc 120	g Pro Asp	gga atc atc Gly Ile Ile 125	atc gcc caa 384 Ile Ala Gln
gac atc c Asp Ile F 130	occ gat ttc Pro Asp Phe	act gtc ccc Thr Val Pro 135	gat tcc Asp Ser	cta ccc cca Leu Pro Pro 140	ttt gtc atc 432 Phe Val Ile
gca ggc a Ala Gly T 145	cc aga atc hr Arg Ile	acc caa gcc Thr Gln Ala 150	agc acc Ser Thr	cat gat tca His Asp Ser 155	gtg gcc aac 480 Val Ala Asn 160
gat gac t Asp Asp P	tc cgg ggc he Arg Gly 165	gca gaa ata Ala Glu Ile	gcc aca Ala Thr 170	aaa cac ctc Lys His Leu	atc gat ctt 528 Ile Asp Leu 175
gga cac a Gly His T	cc cac atc hr His Ile 180	gcc cac cta Ala His Leu	cgc gtg Arg Val 185	gga agc ggc Gly Ser Gly	gct ggc tta 576 Ala Gly Leu 190
Arg Arg F	tc gaa agc he Glu Ser 95	ttt gag gca Phe Glu Ala 200	acc atg Thr Met	cgt gca cat Arg Ala His 205	ggc ctg gag 624 Gly Leu Glu
ccg ctt to Pro Leu Se 210	cc aac gat er Asn Asp	tac ctc ggc Tyr Leu Gly 215	ccc gcc Pro Ala	gtt gag cac o Val Glu His 2 220	gcc ggg tac 672 Ala Gly Tyr
acc gaa ad Thr Glu Th 225	ir red Ara	cta ctc aaa Leu Leu Lys 230	Glu His	ccg gag gtc a Pro Glu Val 1 235	acc gcc att 720 Thr Ala Ile 240
ttc tcc tc Phe Ser Se	ca aac gac der Asn Asp 245	atc acc gcc Ile Thr Ala	atc gga of Ile Gly 2	gca ctc ggt o Ala Leu Gly <i>I</i>	gec gec egt 768 Ala Ala Arg 255
gaa cta go Glu Leu Gl	gt tta cgc o y Leu Arg v 260	gta cct gaa Val Pro Glu	gat cta t Asp Leu S 265	cca ata atc o Ser Ile Ile 0 2	gga tat gac 816 Gly Tyr Asp 270
aac act co Asn Thr Pr 27	o red Ara (caa acc cga Gln Thr Arg 280	ctg atc a Leu Ile A	aac ctc acc a Asn Leu Thr T 285	acc atc gac 864 Thr Ile Asp
gac aac ag Asp Asn Se 290	c atc ggc or Ile Gly V	gtc ggc tac /al Gly Tyr 295	aac gcc g Asn Ala <i>A</i>	gct ctc ttg t Ala Leu Leu I 300	tg ctg agc 912 eu Leu Ser
atg ctt ga Met Leu As 305	b bro era b	gca ccc cac Ala Pro His B10	Pro Glu I	atc atg cat a le Met His T 315	cg ttg cag 960 hr Leu Gln 320

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1022

<210> 446

<211> 333

<212> PRT

<213> Corynebacterium glutamicum

<400> 446

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Ala Gly Val Ser Lys Ser Leu Val Ser Leu Val Leu Arg Gly Ser Pro
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Asn Val Ser Lys Glu Ser Glu Ala Ala Val Lys Thr Ala Ile Lys Lys 35 40 45

Leu Asn Tyr Gln Pro Asn Arg Ala Ala Ser Asp Leu Ala Ala Lys Arg 50 55 60

Thr Gln Leu Ile Ala Val Leu Ile Asp Asp Tyr Ser Asn Pro Trp Phe 65 70 75 80

Ile Asp Leu Ile Gln Ser Leu Ser Asp Val Leu Thr Pro Lys Gly Tyr \$85\$ 90 95

Arg Leu Ser Val Ile Asp Ser Leu Thr Ser Gln Ala Gly Thr Asp Pro 100 105 110

Ile Thr Ser Ala Leu Ser Met Arg Pro Asp Gly Ile Ile Ile Ala Gln 115 120 125

Asp Ile Pro Asp Phe Thr Val Pro Asp Ser Leu Pro Pro Phe Val Ile 130 135 140

Ala Gly Thr Arg Ile Thr Gln Ala Ser Thr His Asp Ser Val Ala Asn 145 150 155 160

Asp Asp Phe Arg Gly Ala Glu Ile Ala Thr Lys His Leu Ile Asp Leu 165 170 175

Gly His Thr His Ile Ala His Leu Arg Val Gly Ser Gly Ala Gly Leu 180 185 190

Arg Arg Phe Glu Ser Phe Glu Ala Thr Met Arg Ala His Gly Leu Glu 195 200 205

Pro Leu Ser Asn Asp Tyr Leu Gly Pro Ala Val Glu His Ala Gly Tyr 210 215 220

Thr Glu Thr Leu Ala Leu Leu Lys Glu His Pro Glu Val Thr Ala Ile 225 230 235 240

Phe Ser Ser Asn Asp Ile Thr Ala Ile Gly Ala Leu Gly Ala Ala Arg 245 250 255

Glu Leu Gly Leu Arg Val Pro Glu Asp Leu Ser Ile Ile Gly Tyr Asp 265 Asn Thr Pro Leu Ala Gln Thr Arg Leu Ile Asn Leu Thr Thr Ile Asp Asp Asn Ser Ile Gly Val Gly Tyr Asn Ala Ala Leu Leu Leu Ser 300 Met Leu Asp Pro Glu Ala Pro His Pro Glu Ile Met His Thr Leu Gln 310 315 Pro Ser Leu Ile Glu Arg Gly Thr Cys Ala Pro Arg Gly 325 <210> 447 <211> 523 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(523) <223> RXN02827 <400> 447 cggtttactt ttatttatcg aatgaatcat gtacatagaa taataagcat taaagggggg 60 gcgggtagga agaagcagcc gtgtcgcata tgcttacttt atg tat gag cag cag 115 Met Tyr Glu Gln Gln 1 aag atc ctt aac gaa gtc agt gaa aaa cgt ctt cag gca atc aaa gat 163 Lys Ile Leu Asn Glu Val Ser Glu Lys Arg Leu Gln Ala Ile Lys Asp 10 20 ttt aca gaa ctg gga tct gga ttc aag att gcg atg cgg gat ctt tcc 211 Phe Thr Glu Leu Gly Ser Gly Phe Lys Ile Ala Met Arg Asp Leu Ser 25 35 att cgc ggt gca ggt aat ctc tta ggt gct cag cag cat gga ttt att 259 Ile Arg Gly Ala Gly Asn Leu Leu Gly Ala Gln Gln His Gly Phe Ile 40 gat gca gtc ggt ttc gat atg tat tct caa atg cta agc gaa gct gtt 307 Asp Ala Val Gly Phe Asp Met Tyr Ser Gln Met Leu Ser Glu Ala Val 55 tnt cgt aaa caa gga aag aat agt caa gtg gag aag ncc nct gtt gag 355 Xaa Arg Lys Gln Gly Lys Asn Ser Gln Val Glu Lys Xaa Xaa Val Glu 70 atc gac cnc ggt gtc gat gcg tat cta cct gaa aca tac gtg gca gat 403 Ile Asp Xaa Gly Val Asp Ala Tyr Leu Pro Glu Thr Tyr Val Ala Asp 90 can cgg cag aaa atc gag atc tat aaa cga att cgt gaa ctt gat tcg 451 Xaa Arg Gln Lys Ile Glu Ile Tyr Lys Arg Ile Arg Glu Leu Asp Ser 105

caa gaa atg cta gat gaa cta gaa gat gat ctg ctc gac cgt ttt gga 499 Gln Glu Met Leu Asp Glu Leu Glu Asp Asp Leu Leu Asp Arg Phe Gly 125 gaa can cca gaa gaa gta gca cat 523 Glu Xaa Pro Glu Glu Val Ala His 135 <210> 448 <211> 141 <212> PRT <213> Corynebacterium glutamicum <400> 448 Met Tyr Glu Gln Gln Lys Ile Leu Asn Glu Val Ser Glu Lys Arg Leu Gln Ala Ile Lys Asp Phe Thr Glu Leu Gly Ser Gly Phe Lys Ile Ala Met Arg Asp Leu Ser Ile Arg Gly Ala Gly Asn Leu Leu Gly Ala Gln 40 Gln His Gly Phe Ile Asp Ala Val Gly Phe Asp Met Tyr Ser Gln Met Leu Ser Glu Ala Val Xaa Arg Lys Gln Gly Lys Asn Ser Gln Val Glu Lys Xaa Xaa Val Glu Ile Asp Xaa Gly Val Asp Ala Tyr Leu Pro Glu Thr Tyr Val Ala Asp Xaa Arg Gln Lys Ile Glu Ile Tyr Lys Arg Ile 105 Arg Glu Leu Asp Ser Gln Glu Met Leu Asp Glu Leu Glu Asp Asp Leu 115 Leu Asp Arg Phe Gly Glu Xaa Pro Glu Glu Val Ala His 135 <210> 449 <211> 564 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(541) <223> RXN02732 <400> 449 agcccttaaa ctctcattct tttgttagac ttgttcacta attacagaca tccaggggct 60 tagattttta acccctgtca taagtttttg ggaaggtcac atg agc gag aat tac Met Ser Glu Asn Tyr

ago Ser	aag Lys	att	gto Val	gtt Val	. Gly	act Thr	gat Asp	gga Gly	tct Ser 15	Lys	ı toğ Ser	tcc Ser	ctt Leu	cta Leu 20	a gca n Ala	163
gtt Val	gaa Glu	cga Arg	gct Ala 25	Ala	cga Arg	atc	gcc Ala	gca Ala 30	gct Ala	ttc Phe	gac Asp	gcc Ala	act Thr	Leu	atc Ile	211
atc Ile	gga Gly	tgt Cys 40	gca Ala	tac Tyr	tac Tyr	gaa Glu	agc Ser 45	aag Lys	gaa Glu	gac Asp	gct Ala	tca Ser 50	gag Glu	act Thr	ttg Leu	259
cgc Arg	cag Gln 55	gat Asp	tct Ser	gta Val	aca Thr	atc Ile 60	ctc Leu	ggc Gly	gat Asp	gat Asp	cct Pro 65	gct Ala	cgt Arg	gaa Glu	aac Asn	307
ctg Leu 70	gac Asp	aag Lys	gca Ala	gca Ala	gat Asp 75	gca Ala	gca Ala	cgc Arg	gct Ala	gtc Val 80	ggc	gca Ala	acc Thr	tcc Ser	atc Ile 85	355
gag Glu	act Thr	gag Glu	gtt Val	cgt Arg 90	act Thr	ggc Gly	act Thr	cca Pro	gtt Val 95	gag Glu	gct Ala	ttg Leu	atg Met	gca Ala 100	atc Ile	403
gtt Val	aat Asn	gat Asp	cac His 105	caa Gln	gct Ala	gac Asp	ctt Leu	ctt Leu 110	gtg Val	gtt Val	ggt Gly	aac Asn	cgt Arg 115	gga Gly	atc Ile	451
ASN	tat Tyr	120	Thr	Gly	Arg	Leu	Leu 125	Gly	Ser	Val	Pro	Ala 130	Asp	gtt Val	gca Ala	499
cgc Arg	caa Gln 135	tca Ser	gac Asp	tgc Cys	gat Asp	gtc Val 140	atg Met	att Ile	gtt Val	cac His	acc Thr 145	gtg Val	agc Ser			541
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	> 45 Ser		Asn	Tvr	Ser	Lvs	Ile	Val	Val	Glv	Thr	Asn	Cl v	202	Tuo	
1				5					10					15		
Ser	Ser :	Leu	Leu 20	Ala	Val	Glu	Arg	Ala 25	Ala	Arg	Ile	Ala	Ala 30	Ala	Phe	
Asp	Ala '	Thr 35	Leu	Ile	Ile	Gly	Cys 40	Ala	Tyr	Tyr	Glu	Ser 45	Lys	Glu	Asp	
Ala	Ser (Glu '	Thr	Leu .	Arg	Gln . 55	Asp	Ser	Val	Thr	Ile 60	Leu	Gly	Asp	Asp	
Pro 65	Ala <i>P</i>	Arg (Glu .	Asn :	Leu . 70	Asp	Lys .	Ala .	Ala	Asp 75	Ala	Ala	Arg	Ala	Val 80	
Gly A	Ala 1	Thr S	Ser	Ile	Glu '	Thr (Glu '	Val 1	Arg	Thr	Gly	Thr	Pro	Val	Glu	

85 90 95

Ala Leu Met Ala Ile Val Asn Asp His Gln Ala Asp Leu Leu Val Val 100 105 110

Gly Asn Arg Gly Ile Asn Tyr Leu Thr Gly Arg Leu Leu Gly Ser Val 115 120 125

Pro Ala Asp Val Ala Arg Gln Ser Asp Cys Asp Val Met Ile Val His 130 135 140

Thr Val Ser 145

<210> 451

<211> 1272

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1249)

<223> RXN01671

<400> 451

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tttttgtacc cgaatttgta cccgaattta aggaatcgct atg aat cat gtt gtt 115

Met Asn His Val Val

1 5

aat ttt gct tca cat ttg gaa gac gca gcc ctg aag caa gcc gaa gct 163 Asn Phe Ala Ser His Leu Glu Asp Ala Ala Leu Lys Gln Ala Glu Ala

act gcc acc atg ccg ttt att tac ccg cat gtg gcg ttg atg cct gat 211
Thr Ala Thr Met Pro Phe Ile Tyr Pro His Val Ala Leu Met Pro Asp
25 30 35

gct cac ttt ggg ctg ggt tcg tcg gtg gga acg gtg ttc ggc acc aag
Ala His Phe Gly Leu Gly Ser Ser Val Gly Thr Val Phe Gly Thr Lys
40
45
50

ggt gcg atc att ccg gcg gct gtg ggt gtg gat ata ggt tgc gga atg 307 Gly Ala Ile Ile Pro Ala Ala Val Gly Val Asp Ile Gly Cys Gly Met

ata gga gtg tgt acc aat tac acg gcc tct gac ctg gag gga cgt gat

Ile Gly Val Cys Thr Asn Tyr Thr Ala Ser Asp Leu Glu Gly Arg Asp

75

ttg gtg acg ctt cgg gat tac atc gag cgg gtg att ccg ttg tct cct
Leu Val Thr Leu Arg Asp Tyr Ile Glu Arg Val Ile Pro Leu Ser Pro
90 95 100

gga aat tac aat tcc acc acc ttg aag gaa acc gcg aag gtg aag gtc
Gly Asn Tyr Asn Ser Thr Thr Leu Lys Glu Thr Ala Lys Val Lys Val
105 110 115

gcg gag ttg gag gaa ctc gcg gag cgc gat ggt gta gat ttg tcg cac 499

							,								•	
Ala	a Gl	u Le 12	u Gl 0	u Gl	u Le	u Ala	a Glu 125	a Aro	g Asp	o Gly	y Val	l Asp 130		ı Se:	r His	
tct Sei	Pro	J 111	g tg r Tr	g aad p Ly:	g cgo s Aro	c caq g Glr 140	ı Lei	g ggt	tcq Y Ser	g ctt Lei	= ggt 1 Gl ₂	/ Gl	a ggt / Gly	aat / Asr	cac n His	547
tto Phe 150	= TT6	ga e Gl	g tte u Le	g tgt u Cys	ctt Leu 155	ı Asp	gag Glu	ttç Lev	g gat 1 Asp	cgg Arg 160	y Val	j tgç Trp	g atç Met	ttt Phe	ttg Leu 165	595
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aag Lys	ato Ile	gcg Ala	g caq a Glr 185	g gcc n Ala	gag Glu	ı tgt ı Cys	aag Lys	aat Asn 190	Glu	gag Glu	ctt Leu	ccc Pro	gat Asp 195	Lys	gat Asp	691
ctt Leu	gcg Ala	tac Tyr 200	Let	g acc l Thr	gag Glu	GJA	act Thr 205	gag Glu	gag Glu	ttt Phe	gag Glu	tct Ser 210	tac Tyr	atc Ile	aag Lys	739
gaa Glu	ctg Leu 215	aat Asn	tgg Trp	gcg Ala	cag Gln	cgt Arg 220	ttt Phe	gcg Ala	ttc Phe	ctc Leu	aac Asn 225	agg Arg	gaa Glu	gaa Glu	atg Met	787
atg Met 230	gac Asp	aga Arg	ttc Phe	gca Ala	cgg Arg 235	gag Glu	ctg Leu	ggt Gly	ttt Phe	ttc Phe 240	gtc Val	gac Asp	aag Lys	cag Gln	ctt Leu 245	835
gaa Glu	gag Glu	gtc Val	gag Glu	cgc Arg 250	atc Ile	aac Asn	tgc Cys	cac His	cat His 255	aac Asn	tac Tyr	acg Thr	gtc Val	cag Gln 260	gag Glu	883
gag Glu	cac His	tac Tyr	ggc Gly 265	gag Glu	acc Thr	att Ile	tgg Trp	ctc Leu 270	acc Thr	cgt Arg	aag Lys	ggt Gly	gcc Ala 275	gtg Val	ttg Leu	931
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tcg Ser	tac Tyr 295	gtg Val	ggc Gly	agt Ser	ggc Gly	aag Lys 300	ggc Gly	aac Asn	gcc Ala	gag Glu	gca Ala 305	ctg Leu	cgg Arg	tcg Ser	gcg Ala	1027
ccg Pro 310	cat His	G]A aaa	gcg Ala	ggc Gly	cgg Arg 315	agg Arg	atg Met	tcg Ser	cgc Arg	aac Asn 320	cag Gln	gct Ala	aaa Lys	aag Lys	cgc Arg 325	1075
ttc Phe	tcg Ser	acg Thr	gcc Ala	gac Asp 330	ctg Leu	gat Asp	tct Ser	Arg	atg Met 335	gcg Ala	ggc Gly	atc Ile	gtc Val	tac Tyr 340	cgg Arg	1123
ccc Pro	ggc	aag Lys	gag Glu 345	tgg Trp	atc Ile	gat Asp	Glu	att Ile 350	ccc Pro	gac Asp	gct Ala	Tyr	aaa Lys 355	gac Asp	atc Ile	1171
gat Asp	cag Gln	gtg Val	atg Met	gcc Ala	gat Asp	gct Ala	gcc (Ala /	gat Asp	ttg Leu	gtg Val	aca Thr	att Ile .	cgc Arg	cat His	aaa Lys	1219

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tgc 1272

<210> 452

<211> 383

<212> PRT

<213> Corynebacterium glutamicum

<400> 452

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Lys Gln Ala Glu Ala Thr Ala Thr Met Pro Phe Ile Tyr Pro His Val $20 \\ 25 \\ 30$

Ala Leu Met Pro Asp Ala His Phe Gly Leu Gly Ser Ser Val Gly Thr 35 40 45

Val Phe Gly Thr Lys Gly Ala Ile Ile Pro Ala Ala Val Gly Val Asp 50 55 60

Ile Gly Cys Gly Met Ile Gly Val Cys Thr Asn Tyr Thr Ala Ser Asp 65 70 75 80

Leu Glu Gly Arg Asp Leu Val Thr Leu Arg Asp Tyr Ile Glu Arg Val 85 90 95

Ile Pro Leu Ser Pro Gly Asn Tyr Asn Ser Thr Thr Leu Lys Glu Thr

Ala Lys Val Lys Val Ala Glu Leu Glu Glu Leu Ala Glu Arg Asp Gly 115 120 125

Val Asp Leu Ser His Ser Pro Thr Trp Lys Arg Gln Leu Gly Ser Leu 130 135 140

Gly Gly Gly Asn His Phe Ile Glu Leu Cys Leu Asp Glu Leu Asp Arg 145 150 155 160

Ala Gln Lys His Ile Lys Ile Ala Gln Ala Glu Cys Lys Asn Glu Glu 180 185 190

Leu Pro Asp Lys Asp Leu Ala Tyr Leu Thr Glu Gly Thr Glu Glu Phe 195 200 205

Glu Ser Tyr Ile Lys Glu Leu Asn Trp Ala Gln Arg Phe Ala Phe Leu 210 220

Asn Arg Glu Glu Met Met Asp Arg Phe Ala Arg Glu Leu Gly Phe Phe 225 235 235

Val Asp Lys Gln Leu Glu Glu Val Glu Arg Ile Asn Cys His His Asn

Tyr Thr Val Gln Glu Glu His Tyr Gly Glu Thr Ile Trp Leu Thr Arg 260 265 270

Lys Gly Ala Val Leu Ala Asp Glu Gly Thr Pro Ala Leu Ile Pro Gly 275 280 285

Ser Met Gly Thr Ala Ser Tyr Val Gly Ser Gly Lys Gly Asn Ala Glu 290 295 300

Ala Leu Arg Ser Ala Pro His Gly Ala Gly Arg Arg Met Ser Arg Asn 305 310 315 320

Gln Ala Lys Lys Arg Phe Ser Thr Ala Asp Leu Asp Ser Arg Met Ala 325 330 335

Gly Ile Val Tyr Arg Pro Gly Lys Glu Trp Ile Asp Glu Ile Pro Asp 340 345 350

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<211> 1137

<212> DNA

<213> Corynebacterium glutamicum

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<223> RXS00671

<400> 453

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Met Leu Ile Ser Gln

1

cgc cca acc atc acc gag gaa ttt gtt aat aac gca cgt tcc cgg ttt Arg Pro Thr Ile Thr Glu Glu Phe Val Asn Asn Ala Arg Ser Arg Phe
10 15 20

gtc atc gag cca ctg gag cca ggt ttt ggc tac acc ctc ggt aac tcc 211
Val Ile Glu Pro Leu Glu Pro Gly Phe Gly Tyr Thr Leu Gly Asn Ser
25 30 35

ctg cgc cgt acc ctg ctg tcc tcc att cct gga gca gca gta acc agc 259
Leu Arg Arg Thr Leu Leu Ser Ser Ile Pro Gly Ala Ala Val Thr Ser
40 45 50

gtc aag att gac ggt gta ctc cac gag ttc acc acc atc agc ggt gtt 307 Val Lys Ile Asp Gly Val Leu His Glu Phe Thr Thr Ile Ser Gly Val 55 60 65

aag gaa gat gtc tct gac atc atc ttg aac atc aag gga ttg gtt ttg 355

Lvs	s Gli	ı Ası	n Va	1 50	r Ac		, Tl.	- T -	7	- 1						
, 0	,				/:	5				80	0				l Leu 85	
tct Ser	tct Ser	gat Asp	t to	c gai r Asi 90	o GI	g cca ı Pro	a gtt D Val	t gti L Val	t ato l Met 95	: Glr	g cto n Lei	g gto ı Val	c aaq L Lys	g gaa s Glu 100	a ggc ı Gly)	403
cca Pro	gga Gly	ı gtt Val	gta L Val	LTni	gca Ala	a ggt a Gly	gac Asp	att Ile 110	e Glr	g cca n Pro	a cca Pro	a gca o Ala	ggd Gly	/ Val	g gag Glu	451
atc Ile	cac His	aac Asn 120	Pro	g gat Asp	ctg Leu	cac His	att Ile 125	: Ala	acc Thr	ctg Leu	aac Asn	gag Glu 130	Thr	gcc Ala	aag Lys	499
att Ile	gag Glu 135	TTE	gag Glu	ctc Leu	atc Ile	gtc Val 140	gag Glu	cgt Arg	gga Gly	cgt Arg	ggc Gly 145	Tyr	gtt Val	ccc Pro	gca Ala	547
act Thr 150	gtt Val	act Thr	gca Ala	acc Thr	ggt Gly 155	gga Gly	gag Glu	atc Ile	ggc Gly	cgc Arg 160	att Ile	ccg Pro	gtc Val	gat Asp	cag Gln 165	595
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gtt Val	gag Glu	cag Gln	cgc Arg 185	acc Thr	gac Asp	ttt Phe	gac Asp	aag Lys 190	ctg Leu	gtc Val	atc Ile	gac Asp	gtt Val 195	gag Glu	acc Thr	691
aag Lys	aac Asn	tct Ser 200	att Ile	acc Thr	gca Ala	cgt Arg	gac Asp 205	gcc Ala	ctg Leu	gcg Ala	tcg Ser	gca Ala 210	ggt Gly	aag Lys	acc Thr	739
ьeu	gtt Val 215	gag Glu	ctg Leu	ttc Phe	ggc Gly	ctc Leu 220	gca Ala	cgc Arg	gag Glu	ctg Leu	aac Asn 225	atc Ile	gca Ala	gcc Ala	gag Glu	787
ggc Gly 230	atc Ile	gag Glu	atc Ile	СŢЪ	cca Pro 235	tct Ser	cct Pro	cag Gln	gag Glu	acc Thr 240	gag Glu	tac Tyr	atc Ile	gct Ala	gcc Ala 245	835
tac Tyr	agc Ser	atg Met	cca Pro	atc Ile 250	gag Glu	gat Asp	ctg Leu	gac Asp	ttc Phe 255	tct Ser	gtc Val	cgt Arg	tcc Ser	tac Tyr 260	aac Asn	883
tgc (Cys :	ctc Leu	aag Lys	cgc Arg 265	gaa Glu	gac Asp	atc Ile	cac His	acc Thr 270	gtg Val	ggt Gly	gaa Glu	ctc Leu	gca Ala 275	gag Glu	cgc Arg	931
gct (3 L U	tcc Ser 280	gat Asp	ttg Leu	ctg Leu	Asp	atc Ile 285	cgc Arg	aac Asn	ttc Phe	gga Gly	cag Gln 290	aag Lys	tcg Ser	atc Ile	979
aac (Asn (gag Glu 295	gta Val	aag Lys	atc Ile	ьys	ctt Leu 300	gct Ala	ggc Gly	ctg Leu	ggt Gly	ctg Leu 305	acc Thr	ctg Leu	aag Lys	gat Asp	1027
gct o Ala E	cct (Pro (gaa Glu	gac Asp	ttc Phe	gat Asp	cct Pro	tca Ser	act Thr	ctt Leu	gaa Glu	ggt Gly	tat Tyr	gac Asp	gcc Ala	gaa Glu	1075

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<210> 454

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 454

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Thr Leu Gly Asn Ser Leu Arg Arg Thr Leu Leu Ser Ser Ile Pro Gly 35 40 45

Ala Ala Val Thr Ser Val Lys Ile Asp Gly Val Leu His Glu Phe Thr 50 60

Thr Ile Ser Gly Val Lys Glu Asp Val Ser Asp Ile Ile Leu Asn Ile 65 70 7.5 80

Lys Gly Leu Val Leu Ser Ser Asp Ser Asp Glu Pro Val Val Met Gln
85 90 95

Leu Val Lys Glu Gly Pro Gly Val Val Thr Ala Gly Asp Ile Gln Pro
100 105 110

Pro Ala Gly Val Glu Ile His Asn Pro Asp Leu His Ile Ala Thr Leu 115 120 125

Asn Glu Thr Ala Lys Ile Glu Ile Glu Leu Ile Val Glu Arg Gly Arg 130 135 140

Gly Tyr Val Pro Ala Thr Val Thr Ala Thr Gly Gly Glu Ile Gly Arg 145 150 155 160

Ile Pro Val Asp Gln Ile Tyr Ser Pro Val Leu Lys Val Ser Tyr Lys 165 170 175

Val Glu Ala Thr Arg Val Glu Gln Arg Thr Asp Phe Asp Lys Leu Val

Ile Asp Val Glu Thr Lys Asn Ser Ile Thr Ala Arg Asp Ala Leu Ala 195 200 205

Ser Ala Gly Lys Thr Leu Val Glu Leu Phe Gly Leu Ala Arg Glu Leu 210 220

Asn Ile Ala Ala Glu Gly Ile Glu Ile Gly Pro Ser Pro Gln Glu Thr 225 230 235 240

Glu Tyr Ile Ala Ala Tyr Ser Met Pro Ile Glu Asp Leu Asp Phe Ser

Val Arg Ser Tyr Asn Cys Leu Lys Arg Glu Asp Ile His Thr Val Gly 260 265 270

Glu Leu Ala Glu Arg Ala Glu Ser Asp Leu Leu Asp Ile Arg Asn Phe 275 280 285

Gly Gln Lys Ser Ile Asn Glu Val Lys Ile Lys Leu Ala Gly Leu Gly 290 295 300

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70 75 80 85

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ctg Leu	gaa Glu 295	gtt Val	ttg Leu	gtg Val	ser	atc Ile 300	ttt Phe	ggt Gly .	cgt Arg	Glu	act Thr 305	cct (Pro	gtt Val	gat Asp	ctc Leu	1027
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Ala Glu Glu Ala Pro Ala Ala Ala Glu Ser Glu Ala Pro Val Glu Glu 65 70 75 80

Asp Glu Glu Ala Asp Ser Leu Ala Gln Ala Ala Ala Ala Leu Gly Asp 85 90 95

Thr Asp Glu Gln Asp Ala Asp Ala Glu Tyr Lys Ala Arg Leu Arg Lys 100 105 110

Phe Thr Arg Glu Leu Lys Lys Gln Pro Gly Val Trp Tyr Ile Ile Gln 115 120 125

Cys Tyr Ser Gly Tyr Glu Asn Lys Val Lys Ala Asn Leu Asp Met Arg

Ala Gln Thr Leu Glu Val Glu Asp Asp Ile Phe Glu Val Val Pro 145 150 155 160

Ile Glu Gln Val Thr Glu Ile Arg Asp Gly Lys Arg Lys Leu Val Lys 165 170 175

Arg Lys Leu Pro Gly Tyr Val Leu Val Arg Met Asp Met Asn Asp 180 185 190

Arg Val Trp Ser Val Val Arg Asp Thr Pro Gly Val Thr Ser Phe Val 195 200 205

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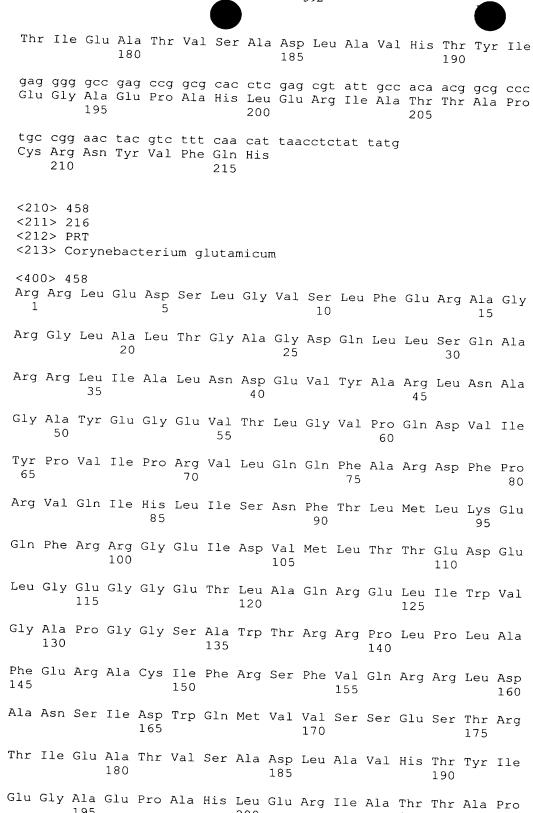
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662



205

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Leu	Val	Arg	Val	Tyr	Leu .	Asn (Gly	Ile	Gly :	Lys	Thr .	Ala :		Leu	Thr	

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Lys Arg Asp Leu Lys Val Leu Ala Lys Asp Gly Lys Lys Ala Arg Ser 85 90 95

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Tyr Thr Gly Arg Gly Met Pro Leu Leu Asp Leu Ile Gln Glu Gly Asn 115 120 125

Leu Gly Leu Ile Arg Ala Met Glu Lys Phe Asp Tyr Ser Lys Gly Phe 130 135 140

Lys Phe Ser Thr Tyr Ala Thr Trp Trp Ile Arg Gln Ala Ile Thr Arg 145 150 155 160

Gly Met Ala Asp Gln Ser Arg Thr Ile Arg Leu Pro Val His Leu Val 165 170 175

Glu Gln Val Asn Lys Leu Ser Arg Ile Lys Arg Glu Leu Tyr Gln His 180 185 190

Leu Gly Arg Glu Ala Thr Asn Glu Glu Leu Ala Glu Glu Ser Gly Ile 195 200 205

Glu Glu Ser Lys Ile Glu Met Leu Leu Arg Gln Ser Arg Asp Pro Val 210 215 220

Ser Leu Asp Met Pro Val Gly Ala Asp Glu Glu Ala Pro Leu Gly Asp 225 230 235 240

Phe Ile Glu Asp Ser Glu Ala Thr Asp Ala Glu Ser Ala Val Val Ala 245 250 255

Ser Met Arg His Ser Asp Ile Arg Ala Val Leu Asn Thr Leu Glu Pro 260 265 270

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Pro Arg Thr Leu Asp Gln Ile Gly Arg Arg Phe Gly Leu Ser Arg Glu 290 295 300

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ctt gcc acc ctt aag gat aaa ggc gag ttt gtt aaa acc gca tca tcc Leu Ala Thr Leu Lys Asp Lys Gly Glu Phe Val Lys Thr Ala Ser Ser

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							acc Thr					-		_	_	307
	_					-	gcg Ala		_	_		-			-	355
	-			-	_		gca Ala	-	_		_		-	_		403
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							ggc Gly									931

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-	-		-	cag Gln		_			_		_					1027
				cca Pro												1075
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				aag Lys												1411
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				gac Asp 490												1603
				gtc Val					Asp						ttg Leu	1651
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Glu His Tyr Gly Ser Ser Gly Ser Asp Lys Ser Asp Thr Ala Ala Lys
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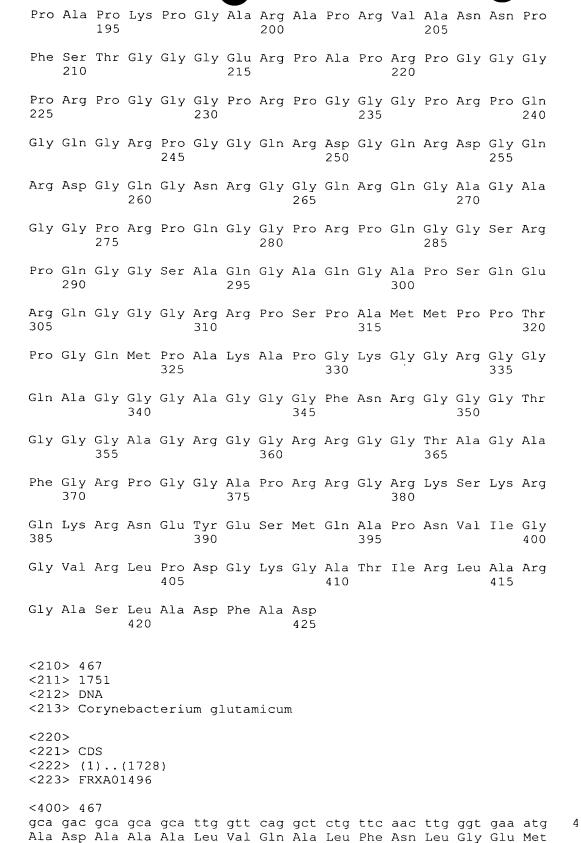
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Leu Ala His Ile Ser Gly Lys Met Arg Gln His Tyr Ile Arg Ile Leu $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$

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Asp His Gly Lys Thr Thr Thr Ala Ala Ile Thr Lys Val Leu Ala
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gac act tac cct gag ctc aac gag gct ttc gcc ttc gac tcc atc gat 259
Asp Thr Tyr Pro Glu Leu Asn Glu Ala Phe Ala Phe Asp Ser Ile Asp
40 45

aag gct cct gag gag aag gag cgt ggc atc acg atc aac atc tcc cac

Lys Ala Pro Glu Glu Lys Glu Arg Gly Ile Thr Ile Asn Ile Ser His

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gac ggc gca atc ctc gtt gtt gct gct acc gac ggc cca atg cct cag 451 Asp Gly Ala Ile Leu Val Val Ala Ala Thr Asp Gly Pro Met Pro Gln 105 110 115

201	12/0							- (015 -							
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Leu	135	Ala	Leu	Asn	Lys	Cys 140	gac Asp	Met	Val	Glu	Asp 145	Glu	Glu	Ile	Ile	547
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Phe Asp Ser Ile Asp Lys Ala Pro Glu Glu Lys Glu Arg Gly Ile Thr

Ile Asn Ile Ser His Val Glu Tyr Gln Thr Glu Lys Arg His Tyr Ala

His Val Asp Ala Pro Gly His Ala Asp Tyr Ile Lys Asn Met Ile Thr

Gly Ala Ala Gln Met Asp Gly Ala Ile Leu Val Val Ala Ala Thr Asp 100

Gly Pro Met Pro Gln Thr Arg Glu His Val Leu Leu Ala Arg Gln Val 120

Gly Val Pro Tyr Ile Leu Val Ala Leu Asn Lys Cys Asp Met Val Glu 135

Asp Glu Glu Ile Ile Glu Leu Val Glu Met Glu Val Arg Glu Leu Leu 150 155

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Leu Lys Ala Leu Glu Gly Asp Glu Lys Trp Gly Lys Gln

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gat aag gct cct Asp Lys Ala Pro 35	gag gag aag Glu Glu Lys	gag cgt ggc Glu Arg Gly 40	atc acg atc Ile Thr Ile 45	aac atc tcc Asn Ile Ser	144
cac gtt gag tac His Val Glu Tyr 50	cag act gaa Gln Thr Glu 55	aag cgc cac Lys Arg His	tac gca cac Tyr Ala His 60	gtt gac gct Val Asp Ala	192
cca ggc cac gcc Pro Gly His Ala 65	gac tac atc Asp Tyr Ile 70	aag aac atg Lys Asn Met	att acc ggc Ile Thr Gly 75	gct gct cag Ala Ala Gln 80	240
atg gac ggc gca Met Asp Gly Ala	atc ctc gtt Ile Leu Val 85	gtt gct gct Val Ala Ala 90	acc gac ggc Thr Asp Gly	cca atg cct Pro Met Pro 95	288
cag acc cgt gag Gln Thr Arg Glu 100	cac gtt ctt His Val Leu	ctt gct cgc Leu Ala Arg 105	cag gtt ggc Gln Val Gly	gtt cct tac Val Pro Tyr 110	336
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atc gag ctc gtc Ile Glu Leu Val 130	gag atg gaa Glu Met Glu 135	gtt cgt gaa Val Arg Glu	ctt ctt gct Leu Leu Ala 140	gag cag gac Glu Gln Asp	432
tac gac gaa gag Tyr Asp Glu Glu 145	gct cca att Ala Pro Ile 150	gtt cac atc Val His Ile	tcc gct ctg Ser Ala Leu 155	aag gct ctt Lys Ala Leu 160	480
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gat ttc aag aac ggt cta gtt ctc aag aac gaa ggc aag ctg cag 163 Asp Phe Lys Asn Gly Leu Val Leu Lys Asn Glu Gly Lys Leu Gln Gln 10 15 20

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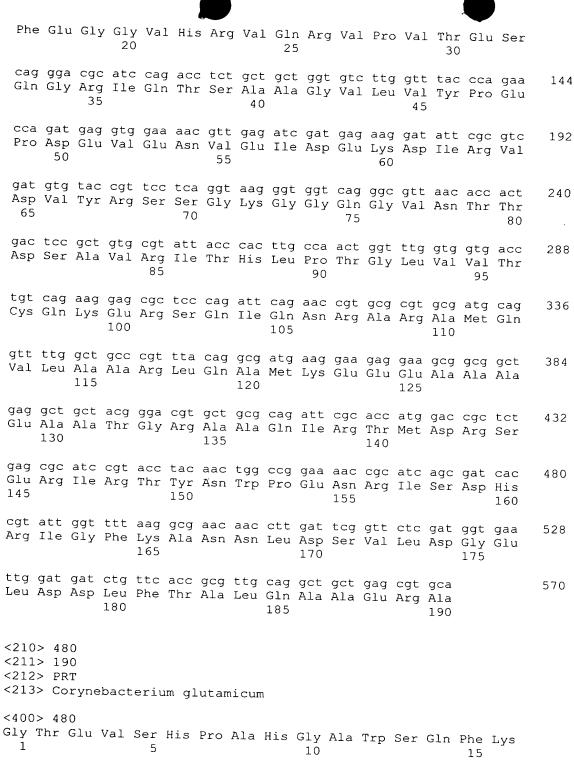
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Gly Pro Ala Phe Val Arg Thr Lys Leu Lys Asp Val Val Thr Gly Lys

Thr Ile Asp Lys Thr Trp Asn Ala Gly Val Lys Val Glu Thr Ala Thr 55

Val Asp Arg Arg Asp Val Thr Tyr Leu Tyr Asn Asp Gly Thr Ser Phe Ile Val Met Asp Asp Lys Thr Phe Glu Gln Tyr Glu Leu Ser Pro Asp 8.5 Ala Phe Gly Asp Ala Gly Arg Phe Leu Leu Glu Asn Met Arg Val Gln 105 Val Ser Phe His Glu Gly Glu Ala Leu Phe Gly Glu Leu Pro Val Ser 115 Val Asp Leu Arg Val Glu His Thr Asp Pro Gly Leu Gln Gly Asp Arg 135 Ser Thr Gly Gly Thr Lys Pro Ala Thr Leu Glu Thr Gly Ala Glu Ile 145 150 155 Gln Val Pro Leu Phe Ile Glu Thr Gly Asn Val Leu Lys Val Asp Thr Arg Asp Gly Ser Tyr Leu Ser Arg Val Asn Asn 180 <210> 477 <211> 480 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(457) <223> RXA00331 <400> 477 cagegeegae eageaagega agtaetgaee eagatttaeg aagaagtget eeceeacete 60 taaaatgcct gttccggcac ttcccttcgg ggaaacagct atg gtt ggc cac atg Met Val Gly His Met tcg aat gat cac cca tac tcc ccc gca aaa cgc gtc gga aat ttc atc 163 Ser Asn Asp His Pro Tyr Ser Pro Ala Lys Arg Val Gly Asn Phe Ile 10 ttc gtc tcc ggc gct ctt tca gta gac aag gac tac caa cca gtc gtc 211 Phe Val Ser Gly Ala Leu Ser Val Asp Lys Asp Tyr Gln Pro Val Val 30 ggt cgt aaa gaa gca gtt gat gca gca ctt gaa cgc atg cgt gaa cgc 259 Gly Arg Lys Glu Ala Val Asp Ala Ala Leu Glu Arg Met Arg Glu Arg 40 ctc gcc acc gct ggt ggt gaa ctc aaa gac gtt gtg aaa ctc act tac 307 Leu Ala Thr Ala Gly Gly Glu Leu Lys Asp Val Val Lys Leu Thr Tyr 55 60 ttt gtc acc gac atc agc ctg cgc gaa gaa tgc aac gag caa ttc cga 355 Phe Val Thr Asp Ile Ser Leu Arg Glu Glu Cys Asn Glu Gln Phe Arg 70 75

gaç Gli	g cat ı His	tto Phe	cto Leu	gaa Glu 90	ı Gış	c cgc ⁄ Arg	ccg Pro	gca Ala	a cgo a Aro	g Sei	ttc Phe	gtg Val	ggt Gl	t gca y Ala 100	a tca a Ser)	403
teg Ser	g ctt Leu	cct Pro	tat Tyr 105	. стА	gca Ala	act Thr	gtg Val	gaa Glu 110	ı Ile	gat Asp	gcg Ala	att	gco Ala 115	a Met	atc Ile	451
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Tyr	Gln	Pro 35	Val	Val	Gly	Arg	Lys 40	Glu	Ala	Val	Asp	Ala 45	Ala	Leu	Glu	
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ttt	gaa	ggt (ggc (gtg	cac	cgt (gtt (cag	cgt	gtg	cct	gtt	act	gaa	tct	96



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Gln Gly Arg Ile Gln Thr Ser Ala Ala Gly Val Leu Val Tyr Pro Glu

Pro Asp Glu Val Glu Asn Val Glu Ile Asp Glu Lys Asp Ile Arg Val

Asp Val Tyr Arg Ser Ser Gly Lys Gly Gly Gln Gly Val Asn Thr Thr Asp Ser Ala Val Arg Ile Thr His Leu Pro Thr Gly Leu Val Val Thr Cys Gln Lys Glu Arg Ser Gln Ile Gln Asn Arg Ala Arg Ala Met Gln 105 Val Leu Ala Ala Arg Leu Gln Ala Met Lys Glu Glu Glu Ala Ala Ala 120 Glu Ala Ala Thr Gly Arg Ala Ala Gln Ile Arg Thr Met Asp Arg Ser 135 Glu Arg Ile Arg Thr Tyr Asn Trp Pro Glu Asn Arg Ile Ser Asp His Arg Ile Gly Phe Lys Ala Asn Asn Leu Asp Ser Val Leu Asp Gly Glu 165 170 Leu Asp Asp Leu Phe Thr Ala Leu Gln Ala Ala Glu Arg Ala 180 185 <210> 481 <211> 480 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(457) <223> RXA00011 <400> 481 gaagttette eegtggtgga aaaagtggae teeatcgaea teeetgatge egatgttege 60 gtcgatgtct accgctcctc cggcccaggt ggtcagtcca gtg aac acc acc gac 115 Val Asn Thr Thr Asp tet gee gtg ege etg ace eac ate eca ace gge ate gtg gtg ace tge 163 Ser Ala Val Arg Leu Thr His Ile Pro Thr Gly Ile Val Val Thr Cys 10 15 caa aac gag aaa toa cag ato caa aac aag goa too gog atg ogt gtt 211 Gln Asn Glu Lys Ser Gln Ile Gln Asn Lys Ala Ser Ala Met Arg Val 30 ctc cag gca aaa ctg ctt gag cgt aaa cgc cag gaa gaa cgc gcc gaa 259 Leu Gln Ala Lys Leu Leu Glu Arg Lys Arg Gln Glu Glu Arg Ala Glu atg gat gcc ctc gga gct gga ggc aat gca tcc tgg ggt aac caa atg 307 Met Asp Ala Leu Gly Ala Gly Gly Asn Ala Ser Trp Gly Asn Gln Met 60 cgt tcc tac gtg ctg cac cct tat caa atg gtg aag gat ctg cgc acc Arg Ser Tyr Val Leu His Pro Tyr Gln Met Val Lys Asp Leu Arg Thr

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Asn Phe Glu Val Asn Asp Pro Gln Lys Val Leu Asp Gly Asp Ile Asp 90 95 100

ggc ctt ttg gaa gca ggt att cgc tgg cga atg gct gag agc cag tcg Gly Leu Leu Glu Ala Gly Ile Arg Trp Arg Met Ala Glu Ser Gln Ser 105 115

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Trp Gly Asn Gln Met Arg Ser Tyr Val Leu His Pro Tyr Gln Met Val 65 70 75 80

Lys Asp Leu Arg Thr Asn Phe Glu Val Asn Asp Pro Gln Lys Val Leu 85 90 95

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Met Arg Pro Glu Phe

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cat c His F																931
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Gly A		lis .95	Arg	Leu	Val	Arg	Ile 200	Ser	Pro	Phe	Asp	Asn 205	Gln	Gly	Arg	

Arg Gln Thr Ser Phe Ala Glu Val Glu Val Leu Pro Val Val Glu Lys 210 215 Val Asp Ser Ile Asp Ile Pro Asp Ala Asp Val Arg Val Asp Val Tyr 235 Arg Ser Ser Gly Pro Gly Gly Gln Ser Ser Glu His His Arg Leu Cys 250 Arg Ala Pro Asp Pro His Pro Asn Arg His Arg Gly Asp Leu Pro Lys 265 Arg Glu Ile Thr Asp Pro Lys Gln Gly Ile Arg Asp Ala Cys Ser Pro 280 Gly Lys Thr Ala 290 <210> 485 <211> 741 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(741) <223> RXN01926 <400> 485 ctg cga agc ttc tac acc cca gaa caa gcc atc gaa cgc gaa ggc gac 48 Leu Arg Ser Phe Tyr Thr Pro Glu Gln Ala Ile Glu Arg Glu Gly Asp 10 gtc tgg aaa gcc gcc acc gaa gaa gca gaa ctc ctc gca gct gac ggc 96 Val Trp Lys Ala Ala Thr Glu Glu Ala Glu Leu Leu Ala Ala Asp Gly 20 25 gcc gtc cac gac cag gaa ctc ttc ctc aac tgc acc acc tcc cca ctg 144 Ala Val His Asp Gln Glu Leu Phe Leu Asn Cys Thr Thr Ser Pro Leu 40 atc ttc gcc tcc gcg atg ctc aac ttc ggc gtc cac caa atc ctg gac 192 Ile Phe Ala Ser Ala Met Leu Asn Phe Gly Val His Gln Ile Leu Asp 50 55 acc ete tge caa ete gea eea tee eee gee gge ege gae gea gae eee 240 Thr Leu Cys Gln Leu Ala Pro Ser Pro Ala Gly Arg Asp Ala Asp Pro 65 70 aaa gee ete gaa gee gee ace tee gea atg gae gae ege gae ace 288 Lys Ala Leu Glu Ala Ala Thr Ser Ala Met Asp Asp His Arg Asp Thr 8.5 acc gac gac ttc tcc ggc gtc gtc ttc aaa gtc caa gcc ggc atg gac 336 Thr Asp Asp Phe Ser Gly Val Val Phe Lys Val Gln Ala Gly Met Asp 100 110 aaa aac cac cgc gat acc ctc gcc ttc atg cgc gtc gtc tcc ggc gaa 384 Lys Asn His Arg Asp Thr Leu Ala Phe Met Arg Val Val Ser Gly Glu 115

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	acc Thr															480
gaa Glu	acc Thr	gcc Ala	ttc Phe	ccc Pro 165	ggc Gly	gac Asp	atc Ile	gtc Val	ggc Gly 170	ctc Leu	gtc Val	aac Asn	gcc Ala	ggc Gly 175	gcc Ala	528
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cca Pro	atg Met	cca Pro 195	aaa Lys	ttc Phe	gcg Ala	cca Pro	gaa Glu 200	cac His	ttc Phe	cgc Arg	atc Ile	ctg Leu 205	cgc Arg	gcc Ala	aaa Lys	624
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tcc Ser 225	gaa Glu	ggt Gly	gtc Val	gtc Val	cag Gln 230	atc Ile	ctc Leu	aag Lys	aac Asn	gac Asp 235	ctg Leu	cgt Arg	ggc Gly	gac Asp	gcc Ala 240	720
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Ala	Val	His 35	Asp	Gln	Glu	Leu	Phe 40	Leu	Asn	Cys	Thr	Thr 45	Ser	Pro	Leu	
Ile	Phe 50	Ala	Ser	Ala	Met	Leu 55	Asn	Phe	Gly	Val	His 60	Gln	Ile	Leu	Asp	
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Lys Ala Leu Glu Ala Ala Thr Ser Ala Met Asp Asp His Arg Asp Thr

Thr Asp Asp Phe Ser Gly Val Val Phe Lys Val Gln Ala Gly Met Asp 100 105 110

Lys Asn His Arg Asp Thr Leu Ala Phe Met Arg Val Val Ser Gly Glu Phe Asp Arg Gly Met Gln Val Thr His Ser Gln Ser Gly Arg Ser Phe 135 Ser Thr Lys Tyr Ala Leu Thr Val Phe Gly Arg Thr Arg Ser Thr Val Glu Thr Ala Phe Pro Gly Asp Ile Val Gly Leu Val Asn Ala Gly Ala Leu Ala Pro Gly Asp Thr Ile Phe Glu Gly Arg Lys Ile Gln Tyr Pro 185 Pro Met Pro Lys Phe Ala Pro Glu His Phe Arg Ile Leu Arg Ala Lys Ser Leu Gly Lys Tyr Lys Gln Phe Arg Lys Ala Leu Glu Gln Leu Asp Ser Glu Gly Val Val Gln Ile Leu Lys Asn Asp Leu Arg Gly Asp Ala Asn Pro Gly His Gly Arg Cys 245 <210> 487 <211> 672 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(672) <223> FRXA01926 <400> 487 ctg cga age tte tae ace cea gaa caa gee ate gaa ege gaa gge gae Leu Arg Ser Phe Tyr Thr Pro Glu Gln Ala Ile Glu Arg Glu Gly Asp 10 gtc tgg aaa gcc gcc acc gaa gaa gca gaa ctc ctc gca gct gac ggc 96 Val Trp Lys Ala Ala Thr Glu Glu Ala Glu Leu Leu Ala Ala Asp Gly 25 gcc gtc cac gac cag gaa ctc ttc ctc aac tgc acc acc tcc cca ctg 144 Ala Val His Asp Gln Glu Leu Phe Leu Asn Cys Thr Thr Ser Pro Leu 40 192 ate the goe too gog atg one and the gge gto call call ate only gad Ile Phe Ala Ser Ala Met Leu Asn Phe Gly Val His Gln Ile Leu Asp 55 240 ace etc tge caa etc gea eea tee eec gee gge ege gae gea gae eec Thr Leu Cys Gln Leu Ala Pro Ser Pro Ala Gly Arg Asp Ala Asp Pro 70 aaa goo oto gaa goo goo aco too goa atg gac gac cac ogo gac aco 288 Lys Ala Leu Glu Ala Ala Thr Ser Ala Met Asp Asp His Arg Asp Thr

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Thr Asp Asp Phe Ser Gly Val Val Phe Lys Val Gln Ala Gly Met Asp

Lys Asn His Arg Asp Thr Leu Ala Phe Met Arg Val Val Ser Gly Glu 115 120 125 Phe Asp Arg Gly Met Gln Val Thr His Ser Gln Ser Gly Arg Ser Phe 135 Ser Thr Lys Tyr Ala Leu Thr Val Phe Gly Arg Thr Arg Ser Thr Val 145 150 155 Glu Thr Ala Phe Pro Gly Asp Ile Val Gly Leu Val Asn Ala Gly Ala Leu Ala Pro Gly Asp Thr Ile Phe Glu Gly Arg Lys Ile Gln Tyr Pro 185 Pro Met Pro Lys Phe Ala Pro Glu His Phe Arg Ile Leu Arg Ala Lys 200 Ser Leu Gly Lys Tyr Lys Gln Phe Arg Lys Ala Leu Glu Gln Leu Asp 215 <210> 489 <211> 478 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(478) <223> RXN02002 <400> 489 aagtggcaaa aaacgtttca agcaggcaac gccggcgtac aacttcgctg agctggggcg 60 attatggccc agcgcccaca acccgctatt cttaataccc atg agc aac gcc aat 115 Met Ser Asn Ala Asn too gac acc acc gcc gcc gag gca cat cgc cgc aga aca ttc gcc gta 163 Ser Asp Thr Thr Ala Ala Glu Ala His Arg Arg Arg Thr Phe Ala Val 10 15 ate gea cae eee gae gee ggt aaa tee aee ete aee gag gea ttg geg 211 Ile Ala His Pro Asp Ala Gly Lys Ser Thr Leu Thr Glu Ala Leu Ala 25 ctg cat gca cac atc atc tcc gaa gcc ggc gcc acc cac ggc aaa gca 259 Leu His Ala His Ile Ile Ser Glu Ala Gly Ala Thr His Gly Lys Ala 40 ggc cgc aaa gcc acc gtt tcc gac tgg atg gaa atg gaa aaa gac cgc 307 Gly Arg Lys Ala Thr Val Ser Asp Trp Met Glu Met Glu Lys Asp Arg ggc atc tcc atc gcc tcc tcc gca ctc caa ttc gag tac gca cca gaa Gly Ile Ser Ile Ala Ser Ser Ala Leu Gln Phe Glu Tyr Ala Pro Glu

85 70 80 ggc cac gca ggc gag ccc ttc atg atc aac ctc gtg gac acc cca ggc 403 Gly His Ala Gly Glu Pro Phe Met Ile Asn Leu Val Asp Thr Pro Gly 90 451 cac gcc gac ttc tcc gaa gac acc tac cgc gtc ctc atg gcc gtc gac His Ala Asp Phe Ser Glu Asp Thr Tyr Arg Val Leu Met Ala Val Asp 105 110 478 gca gca gtc atg ctt atg cac tcc gtc Ala Ala Val Met Leu Met His Ser Val 120 125 <210> 490 <211> 126 <212> PRT <213> Corynebacterium glutamicum <400> 490 Met Ser Asn Ala Asn Ser Asp Thr Thr Ala Ala Glu Ala His Arg Arg Arg Thr Phe Ala Val Ile Ala His Pro Asp Ala Gly Lys Ser Thr Leu 25 Thr Glu Ala Leu Ala Leu His Ala His Ile Ile Ser Glu Ala Gly Ala Thr His Gly Lys Ala Gly Arg Lys Ala Thr Val Ser Asp Trp Met Glu Met Glu Lys Asp Arq Gly Ile Ser Ile Ala Ser Ser Ala Leu Gln Phe Glu Tyr Ala Pro Glu Gly His Ala Gly Glu Pro Phe Met Ile Asn Leu Val Asp Thr Pro Gly His Ala Asp Phe Ser Glu Asp Thr Tyr Arg Val Leu Met Ala Val Asp Ala Ala Val Met Leu Met His Ser Val 120 <210> 491 <211> 394 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (17)..(394) <223> FRXA02002 <400> 491 qctattctta atacccatq aqc aac qcc aat ccc qac acc acc gcc gcc gag Met Ser Asn Ala Asn Pro Asp Thr Thr Ala Ala Glu

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Met Glu Lys Asp Arg Gly Ile Ser Ile Ala Ser Ser Ala Leu Gln Phe 65 70 75 80 Glu Tyr Ala Pro Glu Gly His Ala Gly Glu Pro Phe Met Ile Asn Leu 85 90 95

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Ala Asp Met Tyr Glu Thr Met Asp Val Ala Asn Gly Val Gly Leu Ala $35 \hspace{1cm} 40 \hspace{1cm} 45$

Ala Asn Gln Ile Gly Val Ser Lys Arg Ile Phe Val Tyr Asp Cys Pro 50 55 60

Asp Asp Glu Gly Val Met His Lys Gly Cys Phe Ile Asn Pro Val Leu 65 70 75 80

Glu Thr Ser Glu Ile Pro Glu Thr Met Pro Ala Asp Asp Gly Ser Asp 85 90 95

Glu Glu Gly Cys Leu Ser Val Pro Gly Glu Gly Phe Pro Thr Gly Arg 100 105 110

Ala His Trp Ala Lys Val Thr Gly Leu Asn Glu Lys Gly Glu Glu Val 115 . 120 125

Ser Val Glu Ala Glu Gly Phe Leu Ala Arg Cys Phe Gln His Glu Val 130 135 140

Gly His Leu Asp Gly Phe Leu Tyr Thr Asp Val Leu Ile Gly Arg Trp 145 150 155 160

Lys Arg Met Ala Lys Lys Ala Ile Lys Ala Asn Gly Trp Thr Glu Pro 165 170 175

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	gga gat ccc gta ctt gtg agt Gly Asp Pro Val Leu Val Ser 10	
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	gtg ttc gtg ttt gat acc tcc Val Phe Val Phe Asp Thr Ser 60	
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	aaa gag ggc tgt ttg tcc atc Lys Glu Gly Cys Leu Ser Ile 90 95	3 3 3
	tat gaa acg gtt cgg ctg tct Tyr Glu Thr Val Arg Leu Ser 110	
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	gat cac ctt gat ggc gtg ctg Asp His Leu Asp Gly Val Leu 140	
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gga Gly	gtt Val	gct Ala 120	gct Ala	ctt Leu	gct Ala	cgg Arg	cca Pro 125	cag Gln	ttt Phe	cta Leu	gtc Val	gag Glu 130	atc Ile	tca Ser	gcg Ala	499
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Leu	Pro	PIO	20		Ala	GIU	ALG	25		1 7 1	SCI	1 9 1	30		**** 9	
Ala	Gly	Asp 35		Val	His	Ile	Leu 40		Met	Glu	Ala	Phe 45		Ser	Asp	
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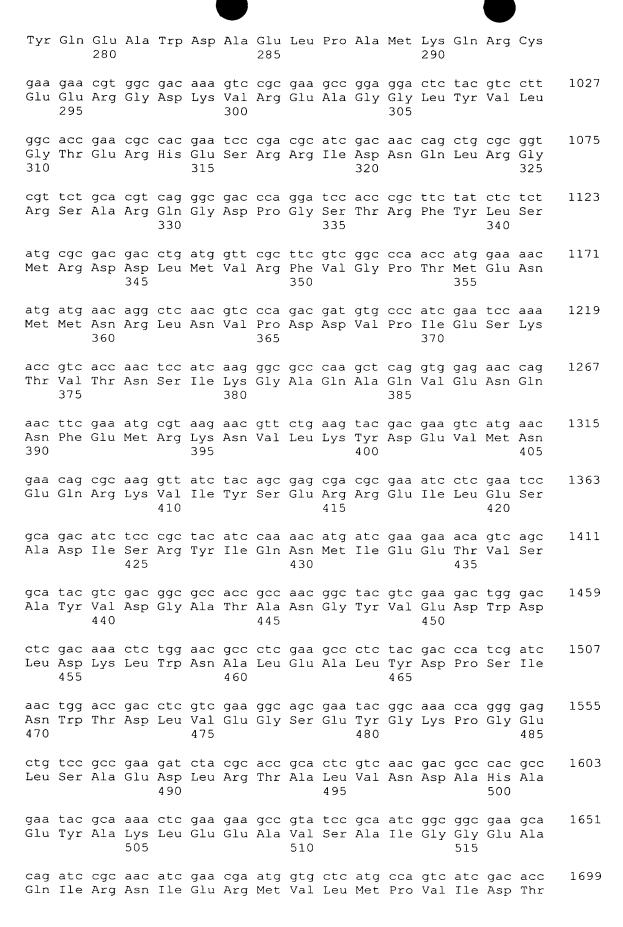
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490

Asn Asp Ala His Ala Glu Tyr Ala Lys Leu Glu Glu Ala Val Ser Ala 505 Ile Gly Gly Glu Ala Gln Ile Arg Asn Ile Glu Arg Met Val Leu Met 515 Pro Val Ile Asp Thr Lys Trp Arg Glu His Leu Tyr Glu Met Asp Tyr Leu Lys Glu Gly Ile Gly Leu Arg Ala Met Ala Gln Arg Asp Pro Leu 550 Val Glu Tyr Gln Lys Glu Gly Gly Asp Met Phe Asn Gly Met Lys Asp 570 Gly Ile Lys Glu Glu Thr Val Arg Gln Leu Phe Leu Ser Ala Ser Ser 580 585 Ser Ser Ser Lys Thr Arg Lys Ser Leu Thr Asn Ser Glu Pro 600 <210> 503 <211> 832 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(832) <223> FRXA00124 <400> 503 tocatoctoa togacquago cogoaccoca otgattatot cogggaccag tagacggous 60 atogoagtto tacaacgtot togoacagat ogtocoacgo atg acc aag gac gtt 115 Met Thr Lys Asp Val 163 cac tac gaa gtc gac gaa cgt aaa aag acc gtc ggt gtg aaa gaa gaa His Tyr Glu Val Asp Glu Arg Lys Lys Thr Val Gly Val Lys Glu Glu 10 211 ggo gto gaa tac gto gaa gao caa oto ggo ato gao aac oto tac goa Gly Val Glu Tyr Val Glu Asp Gln Leu Gly Ile Asp Asn Leu Tyr Ala 25 30 259 cct gag cac tca cag ctg gtc agc tac ctg aac aac gcc atc aag gca Pro Glu His Ser Gln Leu Val Ser Tyr Leu Asn Asn Ala Ile Lys Ala cag gaa ctg ttc acc cgc gac aag gac tac atc gtc cgc aac ggc gaa 307 Gln Glu Leu Phe Thr Arg Asp Lys Asp Tyr Ile Val Arg Asn Gly Glu gtt atg atc gtc gac ggc ttc acc ggc cgt gtc ctt gcc ggc cgc cga 355 Val Met Ile Val Asp Gly Phe Thr Gly Arg Val Leu Ala Gly Arg Arg 70 75 80

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							gcc Ala 125									499
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Gly	Val	Lys	Glu 20	Glu	Gly	Val	Glu	Tyr 25	Val	Glu	Asp	Gln	Leu 30	Gly	Ile	
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Val Arg Asn Gly Glu Val Met Ile Val Asp Gly Phe Thr Gly Arg Val 65 70 75 80

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ctg Leu	aaç Lys	tac Tyr	gad Asp 100) GIU	a gto u Val	atg Met	aac Asr	gaa n Glu 105	ı Glr	g cgo n Aro	c aaq g Lys	g gtt s Val	ato 1110	е Ту	c agc c Ser	336
gag Glu	cga Arg	ege Arg 115	010	ato Ile	ctc Leu	gaa Glu	tcc Ser 120	. ATS	ı gacı Asp	ato Ile	c tco e Ser	c cgc Arg 125	, Tyr	ato Ile	c caa e Gln	384
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Phe Val Gly Pro Thr Met Glu Asn Met Met Asn Arg Leu Asn Val Pro 50 55 60

Asp Asp Val Pro Ile Glu Ser Lys Thr Val Thr Asn Ser Ile Lys Gly
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Ala Gln Ala Gln Val Glu Asn Gln Asn Phe Glu Met Arg Lys Asn Val 85 90 95

Leu Lys Tyr Asp Glu Val Met Asn Glu Gln Arg Lys Val Ile Tyr Ser 100 105 110

Glu Arg Arg Glu Ile Leu Glu Ser Ala Asp Ile Ser Arg Tyr Ile Gln
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Glu Ala Leu Tyr Asp Pro Ser Ile Asn Trp Thr Asp Leu Val Glu Gly 165 170 175

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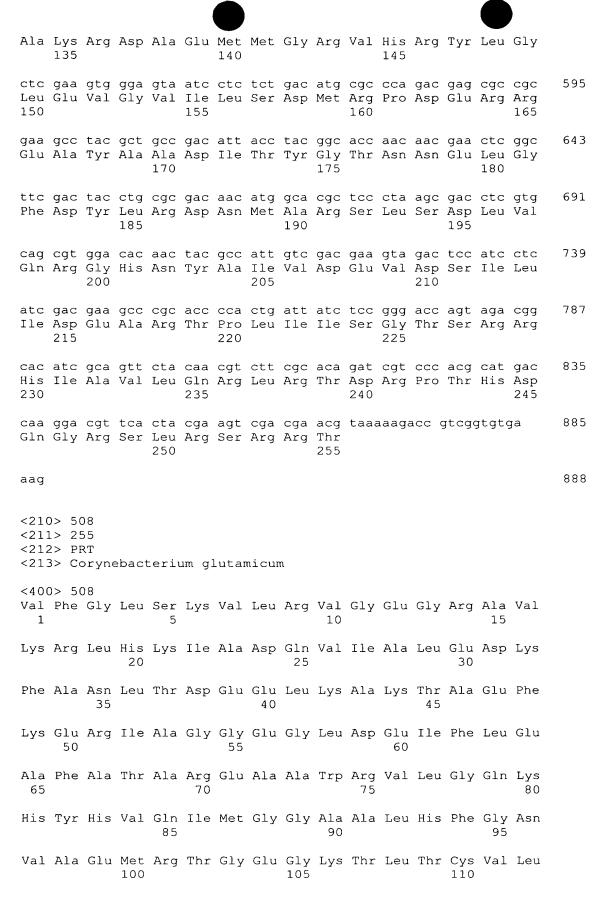
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Asp Pro Leu Val Glu Tyr Gln Lys Glu Gly Gly Asp Met Phe Asn Gly 260 265 270

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Pro Ala Tyr Leu Asn Ala Leu Glu Gly Lys Gly Val His Val Val Thr 120 Val Asn Asp Tyr Leu Ala Lys Arg Asp Ala Glu Met Met Gly Arg Val His Arg Tyr Leu Gly Leu Glu Val Gly Val Ile Leu Ser Asp Met Arg 155 Pro Asp Glu Arg Arg Glu Ala Tyr Ala Ala Asp Ile Thr Tyr Gly Thr Asn Asn Glu Leu Gly Phe Asp Tyr Leu Arg Asp Asn Met Ala Arg Ser Leu Ser Asp Leu Val Gln Arg Gly His Asn Tyr Ala Ile Val Asp Glu Val Asp Ser Ile Leu Ile Asp Glu Ala Arg Thr Pro Leu Ile Ile Ser Gly Thr Ser Arg Arg His Ile Ala Val Leu Gln Arg Leu Arg Thr Asp Arg Pro Thr His Asp Gln Gly Arg Ser Leu Arg Ser Arg Arg Thr <210> 509 <211> 1443 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1420) <223> RXA00687 <400> 509 ttgtaatcgg accaggatct aaagaacaca tctcccggta ccttttagtc actattgtga 60 aaatatgtgg gtttaagtgc tgaggaggcc aggaggataa gtg tcc gcc att att 115 Val Ser Ala Ile Ile cag gca ttc aag gac gcc gat ctg cgt aag aag att ttc ttc act atc 163 Gln Ala Phe Lys Asp Ala Asp Leu Arg Lys Lys Ile Phe Phe Thr Ile 10 1.5 gca atg atc gtt cta tac cgc atc ggt gcg cag atc cct tcc ccg gga 211 Ala Met Ile Val Leu Tyr Arg Ile Gly Ala Gln Ile Pro Ser Pro Gly 30 gtt gac tac gca acg att agt ggt cgt ctg cgt gac ttg act cag gat 259 Val Asp Tyr Ala Thr Ile Ser Gly Arg Leu Arg Asp Leu Thr Gln Asp 40 cag tca age gtt tat tcg ctg att aac ctg ttt tcc ggt gga gcg ctg 307 Gln Ser Ser Val Tyr Ser Leu Ile Asn Leu Phe Ser Gly Gly Ala Leu 55 60 65

	-	cag Gln	_				_				_	_			_		355
		att Ile			-	_	_			_							403
		aag Lys															451
		tac Tyr		_	-	_	_		_	-	-					_	499
		ttg Leu 135		_	-		_	_			-			_		_	547
5		gct Ala						_			_	-	-			_	595
		gca Ala															643
		ggc Gly															691
		cgc Arg				_		-			_						739
		gtt Val 215															787
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		cgc Arg															883
		ttg Leu															931
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		ctg Leu 295	-			_				_	_						1027
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55





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tca atc tcc aac cgt gtc 307 Ser Ile Ser Asn Arg Val

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110

499

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120

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360

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105 110 115 atg gag cca gaa gtt ctt gcg cgc ctt gag cga ttc gtc ggc gtt gac 499 Met Glu Pro Glu Val Leu Ala Arg Leu Glu Arg Phe Val Gly Val Asp 125 ggt gat cgc atc cgc caa atc aac gcg tac tcg cca tca atg gga cgc 547 Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser Pro Ser Met Gly Arg 140 acc att cct cta gtc tgg gtt gtt cca aaa gac aac acc gtg cct tgc 595 Thr Ile Pro Leu Val Trp Val Val Pro Lys Asp Asn Thr Val Pro Cys 155 cca acg gtc tac gca cta 613 Pro Thr Val Tyr Ala Leu 170

<210> 522 <211> 171 <212> PRT <213> Corynebacterium glutamicum

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Asp Pro Asn Met Asn Tyr Asn Pro Ile Asp Asp Ile Lys Asp Arg Pro 50 55 60

Glu Gly Leu Ser Asn Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp 65 70 75 80

Gly Ser Ser Tyr Ala Thr Ala Ser Ser Gly Val Val Thr Ser Ala Leu
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Pro Gln Tyr Thr Asp Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro
100 105 110

Lys Ala Thr Ile Asp Met Glu Pro Glu Val Leu Ala Arg Leu Glu Arg
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Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser 130 135 140

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Leu Ser Ser Met Ser Leu Ile Gly Ser Ser Gln Leu Pro Leu Gly Gly
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Pro Leu Leu Ser Ser Asp Ser Asn Tyr Pro Leu Glu Thr Asp Pro Ser 100 105 110

Ile Thr Glu Ala Arg Ile Val Glu Lys Arg Val Leu Asn Gly Leu Arg 115 120 125

Leu Glu Lys Trp Ser Val Ala Ser Pro Ser Met Gln Arg Asn Val Asp 130 135 140

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Tyr Met Leu Asp Gly Ile Gly Gly Asn Lys Asn Ser Ser Gly Trp Ile 165 170 175

Asn Gly Gly Glu Gly Pro Lys Val Phe Ala Asp Glu Asn Val Thr Val 180 185 190

Val Met Pro Leu Gly Ala Ala Ser Ser Met Tyr Ser Asp Trp Leu Glu 195 200 205

Glu Asp Pro Ala Leu Gly Arg Ile Lys Trp Glu Thr Phe Ile Val Glu 210 215 220

Glu Leu Ala Pro Leu Leu Glu Ala Glu Glu Glu Leu Asn Phe Asn Gly 225 230 235 240

His Arg Gly Ile Gly Gly Leu Ser Met Gly Ala Thr Gly Ala Val His
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Leu Ala Asn Ser Asn Pro Asp Leu Phe Asp Gly Val Ile Gly Ile Ser 260 265 270

Gly Cys Tyr Ser Thr Leu Asp Pro Ile Gly Gln Thr Thr Val Ser Leu 275 280 285

Ile Val Asn Ser Arg Gly Gly Asn Val Glu Asn Met Trp Gly Pro Thr 290 295 300

Gly Ser Glu Thr Trp Lys Ala His Asp Val Thr Ser Asn Pro Glu Gly 305 310 315 320

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<211> 329

<212> PRT

<213> Corynebacterium glutamicum

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Gly Ala Trp Glu Met Thr Gly Phe Ile Glu Glu Val Trp Lys Met Arg 100 $$ 105 $$ 110

Gly Gly Leu Asp Ser Gln Trp Gly Tyr Pro Thr Ser Ala Pro Val Leu 115 120 125

Asp Ser Asp Ala Pro Val Glu Ile Ala Gln Asn Phe Ser Gly Gly Val 130 135 140

Phe Asp Leu Ala Thr Glu Ile Glu Asp Ala Gly Phe Ser Pro Ile Glu 145 150 155 160

Asp Lys Glu Met Ser Asn Leu Ile Leu Glu Tyr Phe Gly Tyr Leu Gly 165 170 175

Phe Asp Phe Pro Gly Ser Ser Ser Arg Glu Leu Val Gln Asp His Ser 180 185 190

Lys Ser Asp Leu Met Thr Leu Arg Ala Ser Arg Cys Ala Leu Lys Asp 195 200 205

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Tyr Trp Gly Cys Leu Asp Lys Ser Asp Arg Pro Asp Pro Asp Ala Tyr 225 230 235 235

Gly Arg His Asp Tyr Cys Thr Leu Ser Pro Asp Ser Tyr Gly Pro Leu 245 250 255

Gly Lys Lys Ala Glu Phe Ser Gly Ala Cys Ala Arg His Asp Leu Cys 260 265 270

Met Asp Ala Val Asp Ala Asn Gly Thr Gly Tyr Ala Pro Cys His Pro 275 280 285

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m.	- 17-	1 0-		-	_)	
тy	21.	1 Se. 5	r Se	r GL	y Asr	1 Gly 220	/ Ala	a Asp	o Asp	Ph∈	e Gly 225		s Glu	ı Gly	, Ser	
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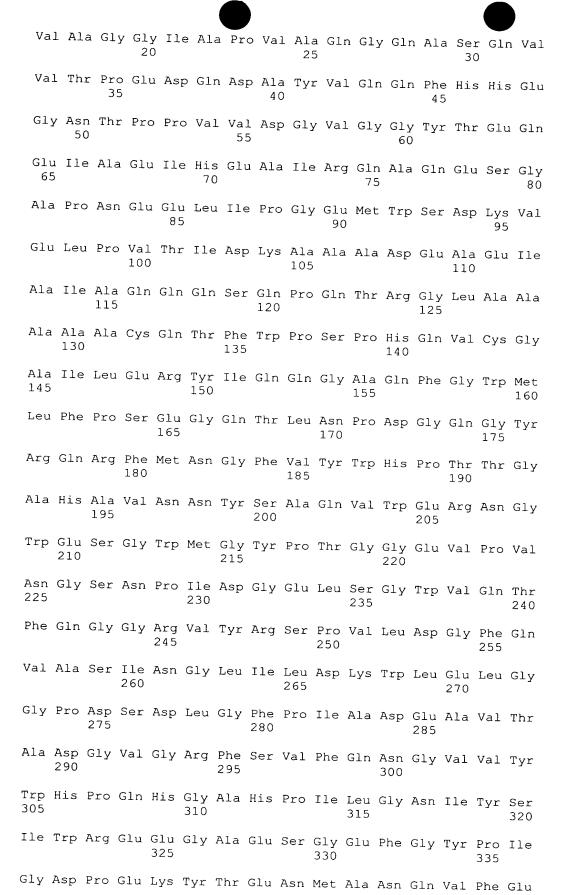
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Ser Lys Lys Tyr Ala Glu Asp Gly Ile Phe Ala Gln Leu Gly Phe Pro 470 Thr Gly Asn Glu Lys Leu Ile Asn Gly Gly Ala Phe Gln Glu Phe Glu 485 Lys Gly Asn Ile Tyr Trp Ser Ala Ser Thr Gly Ala His Val Ile Leu His Gly Asp Ile Phe Asp Ala Trp Gly Ala Lys Gly Trp Glu Gln Gly 520 Glu Tyr Gly Phe Pro Thr Ser Asp Gln Thr Ala Ile Thr Ala Gly Gly 535 Gln Thr Ile Asp Phe Gln Asn Gly Thr Ile Arg Gln Val Asn Gly Arg 550 Ile Glu Glu Ser Arg 565 <210> 535 <211> 1704 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1681) <223> RXN03054 <400> 535 ggtggaaata cgcgcacaac aattttattc acagaactta tgattttttc gggttagggt 60 cagtttgttc acatcaacta gtaacgaaag gatcatgtga atg aaa ctg ttt tcc 115 Met Lys Leu Phe Ser aag gct gca ggc gtc att gct gca gca ctt ctt gtt gca ggt ggt ata 163 Lys Ala Ala Gly Val Ile Ala Ala Ala Leu Leu Val Ala Gly Gly Ile gca cct gtg gca cag ggg caa gct agt cag gtg gtc aca cct gaa gac 211 Ala Pro Val Ala Gln Gly Gln Ala Ser Gln Val Val Thr Pro Glu Asp 30 caa gat gcg tat gtt caa cag ttc cac cac gaa ggg aat acc cca cct 259 Gln Asp Ala Tyr Val Gln Gln Phe His His Glu Gly Asn Thr Pro Pro 40 45 gtg gta gac ggg gtg ggt ggc tac act gag caa gaa atc gcc gag atc 307 Val Val Asp Gly Val Gly Gly Tyr Thr Glu Gln Glu Ile Ala Glu Ile 60 cac gag gct atc cga caa gcc caa gaa tct ggc gca cct aat gaa gag 355 His Glu Ala Ile Arg Gln Ala Gln Glu Ser Gly Ala Pro Asn Glu Glu 8.0 ctc att ccg ggt gag atg tgg tca gat aag gtg gag ctg cca gta act 403 Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val Glu Leu Pro Val Thr

90 95 100 att gat aaa gca gcc gct gat gag gca gag ata gct att gca cag caa 451 Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile Ala Ile Ala Gln Gln 105 caa tot cag cca cag acg cga ggc ctt gct gcg gct gcg gcg tgt cag 499 Gln Ser Gln Pro Gln Thr Arg Gly Leu Ala Ala Ala Ala Cys Gln 120 acg ttt tgg ccg tca cct cat cag gtt tgt ggt gct att tta gag cgc 547 Thr Phe Trp Pro Ser Pro His Gln Val Cys Gly Ala Ile Leu Glu Arg 135 tat att cag cag ggt gcc cag ttt ggg tgg atg ttg ttt ccg agt gaa 595 Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met Leu Phe Pro Ser Glu 150 ggc caa acg tta aat cct gat ggt cag ggg tat cgt cag cgg ttt atg 643 Gly Gln Thr Leu Asn Pro Asp Gly Gln Gly Tyr Arg Gln Arg Phe Met 170 175 aat ggg ttt gtt tat tgg cat ccg aca act ggt gcg cat gct gtt aat 691 Asn Gly Phe Val Tyr Trp His Pro Thr Thr Gly Ala His Ala Val Asn 185 aat tac agt gcg cag gtg tgg gag cgt aat ggg tgg gag tct ggg tgg 739 Asn Tyr Ser Ala Gln Val Trp Glu Arg Asn Gly Trp Glu Ser Gly Trp 200 atg ggt tat ccc act ggt ggt gaa gtc cct gtg aat ggt tcc aat ccg 787 Met Gly Tyr Pro Thr Gly Gly Glu Val Pro Val Asn Gly Ser Asn Pro 215 220 att gat ggt gag ttg agt ggg tgg gtg caa act ttc caa ggt ggg cga 835 Ile Asp Gly Glu Leu Ser Gly Trp Val Gln Thr Phe Gln Gly Gly Arg 235 gtg tat cgc agt ccg gta ttg gac ggt ttc cag gtg gcc agt att aat 883 Val Tyr Arg Ser Pro Val Leu Ásp Gly Phe Gln Val Ála Ser Ile Asn 250 ggg ctg atc ttg gat aaa tgg ctt gaa ttg ggt ggt cct gat agt gac 931 Gly Leu Ile Leu Asp Lys Trp Leu Glu Leu Gly Gly Pro Asp Ser Asp 265 ctt ggt ttt ccc att gcg gat gag gct gtg aca gct gac ggt gtg ggt 979 Leu Gly Phe Pro Ile Ala Asp Glu Ala Val Thr Ala Asp Gly Val Gly 280 285 aga ttt tct gtt ttc cag aac gga gtt gtc tac tgg cat ccg caa cac 1027 Arg Phe Ser Val Phe Gln Asn Gly Val Val Tyr Trp His Pro Gln His 295 300 gga gct cac cct ata tta ggg aat ata tac agt atc tgg aga gaa gaa Gly Ala His Pro Ile Leu Gly Asn Ile Tyr Ser Ile Trp Arg Glu Glu 310 315 gga gct gag agt ggg gaa ttc ggt tac cct atc ggc gat cca gaa aag Gly Ala Glu Ser Gly Glu Phe Gly Tyr Pro Ile Gly Asp Pro Glu Lys 330

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345

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cac His 70	gag Glu	gct Ala	atc Ile	cga Arg	caa Gln 75	gcc Ala	caa Gln	gaa Glu	tct Ser	ggc Gly 80	gca Ala	cct Pro	aat Asn	gaa Glu	gag Glu 85	355
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GJ À āāā	ctg Leu	atc Ile	ttg Leu 265	gat Asp	aaa Lys	tgg Trp	ctt Leu	gaa Glu 270	ttg Leu	ggt Gly	ggt Gly	cct Pro	gat Asp 275	agt Ser	gac Asp	931

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<211> 277

<212> PRT

<213> Corynebacterium glutamicum

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Val Thr Pro Glu Asp Gln Asp Ala Tyr Val Gln Gln Phe His His Glu 35 40 45

Gly Asn Thr Pro Pro Val Val Asp Gly Val Gly Gly Tyr Thr Glu Gln 50 55 60

Glu Ile Ala Glu Ile His Glu Ala Ile Arg Gln Ala Gln Glu Ser Gly 65 70 75 80

Ala Pro Asn Glu Glu Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val 85 90 95

Glu Leu Pro Val Thr Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile 100 105 110

Ala Ile Ala Gln Gln Gln Ser Gln Pro Gln Thr Arg Gly Leu Ala Ala 115 120 125

Ala Ala Cys Gln Thr Phe Trp Pro Ser Pro His Gln Val Cys Gly 130 135 140

Ala Ile Leu Glu Arg Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met 145 150 155 160

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Asn Gly Ser Asn Pro Ile Asp Gly Glu Leu Ser Gly Trp Val Gln Thr 225 230 235 240

Phe Gln Gly Gly Arg Val Tyr Arg Ser Pro Val Leu Asp Gly Phe Gln 245 250 255

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Gly Pro Asp Ser Asp 275

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Glu Asp Asn Thr Val Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly G5 70 75 80

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Glu Leu Thr Ser Glu Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly 100 105 110

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Gly Ala Gln Gln Trp Glu Thr Phe Leu Met His Glu Xaa Xaa Glu Pro 130 135 140

Leu Glu Ala Ala Ile Gly Ala Asp Gly Gln Arg Ser Ile Val Gly Met 145 150 155 160

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768

809

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Ser Leu Met Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Glu Lys 50 55 60

Gly Ile Leu Gly Pro Glu Leu Met Glu Asn Met Arg Ala Gln Ala Glu 65 70 75 80

Arg Phe Gly Thr Asp Met His Met Glu Leu Val Asp Arg Val Asp Leu 85 90 95

Thr Gly Asp Ile Lys Lys Leu Trp Val Gly Asp Asp Glu Tyr His Ala 100 105 110

Arg Ala Val Ile Leu Ser Met Gly Ser Ala Pro Arg Tyr Leu Gly Val 115 120 125

Lys Gly Glu Gln Glu Leu Leu Gly Arg Gly Val Ser Ala Cys Ala Thr 130 135 140

Cys Asp Gly Phe Phe Phe Arg Asp Gln Asp Ile Ala Val Ile Gly Gly 145 150 155 160

Gly Asp Ser Ala Met Glu Glu Ala Thr Phe Leu Thr Lys Phe Ala Arg 165 170 175

Ser Val Thr Ile Val His Arg Arg Glu Glu Phe Arg Ala Ser Ala Ile 180 185 190

Met Leu Glu Arg Ala Gln Lys Asn Glu Lys Ile Arg Phe Val Thr Asn 195 200 205

Lys Thr Val Glu Glu Val Ile Glu Ala Asp Gly Lys Val Ser Gly Leu 210 215 220

Lys Leu Asn Asp Thr Val Thr Gly Glu Asp Ser Val Leu Asp Val Thr 225 230 235 240

Ala Met Phe Val Ala Ile Gly His Asp Pro Arg Ser Glu Ile Leu Ala 245 250 255

Gly Gln Val Glu Val Asp Pro Ser Asn Tyr Val Leu Val Gln Glu Pro 260 265 270

Ser Thr Arg Thr Asn Leu Asp Gly Val Phe Ala Ala Gly Asp Leu Val

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cca acc tac gag aag gtt tcc gaa acc cac acc gac gca acc ttc gcc 259
Pro Thr Tyr Glu Lys Val Ser Glu Thr His Thr Asp Ala Thr Phe Ala
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Lys Leu Asp Thr Glu Ala Asn Gln Gly Leu Ala Ala Ala Leu Gln Ile
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60

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10 15 20

gat gcg cgc cag aag gcc cat gag cag ggg ccg gta act cag ggc att 211
Asp Ala Arg Gln Lys Ala His Glu Gln Gly Pro Val Thr Gln Gly Ile
25 30 35

gct agt tcc ctt gat gtg acc atg gag aac ctg gag aat gag gtg ctg 259
Ala Ser Ser Leu Asp Val Thr Met Glu Asn Leu Glu Asn Glu Val Leu
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Pro	gaa Glu	ctc Leu	aac Asn 105	gtc Val	att Ile	ggc Gly	gtg Val	cat His 110	gca Ala	gac Asp	caa Gln	aac Asn	gca Ala 115	Ala	aac Asn	451
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ccg Pro	cag Gln	cct Pro	ttc Phe	gaa Glu 170	acc Thr	atc Ile	gat Asp	gac Asp	ctc Leu 175	gaa Glu	acc Thr	gct Ala	gtg Val	gca Ala 180	Gly	643
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125

120

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145 150 155 160 Pro Leu Lys Ala Lys Leu Lys Leu Tyr Glu Gln Met Ile Ser Asn Ala 170 Arg Thr Leu Ser Glu Gln Gly Met Phe Val Ser Ala Glu Thr Met Leu 185 Asn Gln Ser Thr Leu Pro His Leu Arg Lys Ile His Gln Glu Val Val His Asp Met Lys Cys Ser Arg His Glu Ile His Pro Met Tyr Pro Ala 215 Asp Phe Ala Ser Gln Leu Asn Val Leu Thr Leu Ala Glu Met Lys Lys 230 235 Thr Ile His Asp Ile Leu Asp Phe Arg Asp Glu Asp Ile Trp Met Leu 245 250 Phe Gly Thr Leu Pro Val Phe Pro Cys Leu Lys Asp Asp Glu Asp Gln 265 Lys Leu Leu Ser Arg Leu Arg Asn Ala Asn Asn Val Thr Thr Arg Asn 280 Asp Pro Asp Gly Arg Ser Arg Leu Asn Val Asn Val Phe Thr Gly Asn 295 Val Ile Val Thr Asp Phe Gly Asp Glu Thr Gly Thr Ile Ser Asn Ile 315 310 Gln Lys Asp Lys Leu Thr Asp Val Phe Asp Lys Trp Leu Ser Ser Asp 325 330 Leu Ala Lys Ser Leu Asn Cys His Cys Ser Glu Phe Ser Cys Leu Gly 340 345 Pro Asn Val Leu Val Lys Asn Met Tyr Tyr Pro Asn Met Asp Phe Lys 360 Asp Asn Glu Arg His Met His Lys Gln Pro Gln Ile Ile Gln Phe 370 375 380 <210> 563 <211> 888 <212> DNA <213> Corynebacterium glutamicum <220>

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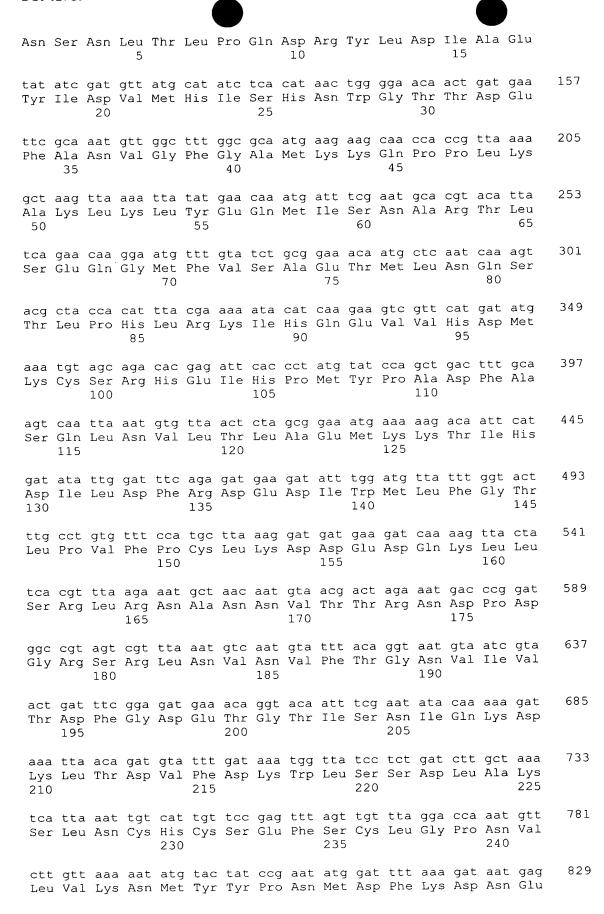
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Glu Phe Ala Asn Val Gly Phe Gly Ala Met Lys Lys Gln Pro Pro Leu 35 40 45

Lys Ala Lys Leu Lys Leu Tyr Glu Gln Met Ile Ser Asn Ala Arg Thr 50 55 60

Leu Ser Glu Gln Gly Met Phe Val Ser Ala Glu Thr Met Leu Asn Gln 65 70 75 80

Ser Thr Leu Pro His Leu Arg Lys Ile His Gln Glu Val Val His Asp \$90\$

Met Lys Cys Ser Arg His Glu Ile His Pro Met Tyr Pro Ala Asp Phe 100 105 110

Ala Ser Gln Leu Asn Val Leu Thr Leu Ala Glu Met Lys Lys Thr Ile 115 120 125

His Asp Ile Leu Asp Phe Arg Asp Glu Asp Ile Trp Met Leu Phe Gly
130 135 140

Thr Leu Pro Val Phe Pro Cys Leu Lys Asp Asp Glu Asp Gln Lys Leu 145 150 155 160

Leu Ser Arg Leu Arg Asn Ala Asn Asn Val Thr Thr Arg Asn Asp Pro 165 170 175

Asp Gly Arg Ser Arg Leu Asn Val Asn Val Phe Thr Gly Asn Val Ile $180 \hspace{1cm} 185 \hspace{1cm} 190 \hspace{1cm}$

Val Thr Asp Phe Gly Asp Glu Thr Gly Thr Ile Ser Asn Ile Gln Lys 195 200 205

Asp Lys Leu Thr Asp Val Phe Asp Lys Trp Leu Ser Ser Asp Leu Ala 210 215 220

Lys Ser Leu Asn Cys His Cys Ser Glu Phe Ser Cys Leu Gly Pro Asn 225 230 235 240

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Glu Arg His Met His Lys Gln Pro Gln Ile Ile Gln Phe $260 \hspace{1cm} 265 \hspace{1cm}$

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gct gtc gcg ctc ggc cgc tca ctg cgc agt gtc atc gtc atc gac gct 21 Ala Val Ala Leu Gly Arg Ser Leu Arg Ser Val Ile Val Ile Asp Ala 25 30 35	.1													
ggt caa ccc cgt aac agc tat gcg cac gct gct cac aat gtc ctc ggc 25 Gly Gln Pro Arg Asn Ser Tyr Ala His Ala Ala His Asn Val Leu Gly 40 45 50	,9													
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	agc Ser															691
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Asp Asp Ala Ser Leu Leu His Ser Arg Arg Ile Ile Leu Ala His Gly $100 \hspace{1cm} 105 \hspace{1cm} 110$

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Thr Lys Val Leu His Cys Ala Tyr Cys His Gly Phe Glu Ala Arg Asp 130 135 140

Ser Glu Ile Val Val Gly Thr Ser Pro Met Ala Ala His Gln Ala 145 150 155 160

Leu Met Phe Ser Gln Leu Ser Lys Thr Val Ser Leu Val Gly Thr Ile 165 170 175

Asp Ile Asp Glu Gln Thr Ser Glu Ser Leu Asp Ser Ala Gly Val Lys 180 185 190

Val Leu Gly Thr Asn Ala Val Arg Val Ser Ala Glu Gly Asp Gly Leu 195 200 205

Ser Val Glu Leu Ser Glu Gly Asp His Leu Ser Cys Asp Asn Ile Val 210 215 220

Val Ala Ser Arg Pro Leu Val Asp Gly Thr Leu Tyr Thr Gln Leu Gly 225 230 235 240

Gly Gln Met Glu Glu Asn Pro Met Gly Arg Phe Ile Pro Gly Thr Gln 245 250 255

Thr Gly Arg Thr Pro Ile Glu Gly Val Trp Ala Ala Gly Asn Ala Gln 260 265 270

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Ser Glu Gly Pr 65	o Phe Tyr 70	Asn Gly S	Ser Val Phe 75	His Arg Val	Ile Asp 80
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Pro Gly Tyr Th:	r Phe Ala	Asp Glu P	he His Pro 05	Glu Leu Arg 110	Phe Asp
Arg Ala Tyr Let 115	leu Ala	Met Ala A 120	sn Ala Gly	Pro Gly Thr 125	Asn Gly
Ser Gln Phe Phe	e Ile Thr	Val Thr Pi 135	ro Thr Pro	His Leu Asn	Asn Ala
His Thr Ile Phe	e Gly Glu '	Val Thr As	sp Ala Glu 155	Ser Gln Lys	Val Val 160
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cgg gac cgc aaa Arg Asp Arg Lys 25	gaa aag a Glu Lys T	cc aag cc hr Lys Pr	o Leu Thr V	gtg gtc ttt d Val Val Phe 2 35	gct tcc 211 Ala Ser

ctg gct gtc atc ctg gtt gtc gtt ggc ggt atc tgg tac gca gct acc Leu Ala Val Ile Leu Val Val Gly Gly Ile Trp Tyr Ala Ala Thr

40

cgo Aro	ago g Ser 55	Ini	gaa Glu	gac Asp	ga <i>a</i> Glu	gto Val	. Ile	acc Thr	gct Ala	gat Asp	gaa Glu 65	Thi	tco Ser	aco Thi	acc Thr	307
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ASII	215	GīĀ	gct Ala	Asp	Thr	Asn 220	Gly	Leu	Pro	Val	Leu 225	Pro	Gln	Leu	Arg	787
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Glu Thr Ser Thr Thr Ala Glu Thr Pro Asp Tyr Gln Pro Leu Ala Leu 65 70 75 80

Thr Arg Thr Thr Ala Leu Gly Asp Ser Val Thr Cys Glu Tyr Pro Asp
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Ala Gly Glu Ala Ser Lys Asp Val Ser Lys Pro Ala Thr Glu Asn Val 100 105 110

Pro Ala Thr Gly Thr Val Thr Val Asn Leu Thr Thr Ala Gln Gly Asn 115 120 125

Ile Gly Met Glu Leu Asp Arg Ser Val Ser Pro Cys Thr Val Asn Ala 130 135 140

Val Glu His Met Ala Ser Glu Gly Tyr Tyr Asn Asp Thr Val Cys His 150 155 160

Arg Ile Thr Thr Ser Gly Ile Tyr Val Leu Gln Cys Gly Asp Pro Ser 165 170 175

Ser Thr Gly Ala Gly Gly Pro Gly Phe Ser Phe Ala Asn Glu Tyr Pro 180 185 190

Thr Asp Glu Ala Thr Asp Leu Thr Thr Pro Val Ile Tyr Glu Arg Gly 195 200 205

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gaa g Glu G	gc :	ctt Leu	gca Ala 100	acc Thr	ctc Leu	gac Asp	gcc Ala	atc Ile 105	gca Ala	gaa Glu	gtt Val	ggc Gly	act Thr 110	gaa Glu	ggt Gly	336
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Gly Pr	:0 G	35	Phe	Ser	Phe	Ala .	Asn 40	Glu	Tyr	Pro	Thr	Asp 45	Glu	Ala	Thr	
Asp Le	eu T	hr :	Thr	Pro '	Val	Ile 55	Tyr	Glu	Arg	Gly	Thr 60	Ile	Ala	Met	Ala	

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gag Glu	ggt Gly	ggc Gly	ctg Leu	gtc Val 250	aag Lys	ctt Leu	gat Asp	gtg Val	ccg Pro 255	acc Thr	gat Asp	tgc Cys	gat Asp	gtc Val 260	att Ile	883
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ctg c Leu G 310	3711	эт	ьeu	AIA	315	Thr	Lys	Asn	Phe	Leu 320	Val	Leu	Thr	Leu	Leu 325	1075
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201	. ++2															
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gcg c	ge d	ctt t	tt.	gct	caa q	gct 1	ttg d	ctt q	gat	gcg (ggc	cag	gcc	gtg	gat	1987

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Trp Lys Arg Gly Thr Pro Leu Glu Gln Ala Glu Leu Phe Phe Glu Gly 200

Ser Arg Gln Asp Val Ala Thr His Ala Trp Arg Asp Ser Thr Pro Gly 215 Phe Glu Arg Thr Phe Val Ser Arg Ser Leu Asp Phe Tyr Asn Ser Glu 230 Thr Ser Leu Glu Thr Glu Gly Gly Leu Val Lys Leu Asp Val Pro Thr 250 Asp Cys Asp Val Ile Val Lys Lys Gln Trp Ile Phe Val Ser Pro Arg Thr Asp Phe Ala Gly Ile Pro Ala Gly Gly Leu Gly Val Leu Leu Lys Glu Phe Leu Glu Gly Gly Arg Asp Phe Gln Pro Val Phe Thr Pro Thr Glu Ser Thr Ser Leu Gln Gly Leu Ala Thr Thr Lys Asn Phe Leu 310 315 Val Leu Thr Leu Leu Asn Asn Val Ser Thr Glu Ile Val Thr Val Pro 325 Leu Asn Asp Pro Thr Thr Glu His Glu His Ile Asp Leu Pro Glu His 345 Val Thr Ala His Val Val Ala Thr Ser Pro Leu Asp Gly Asp Glu Ile Trp Val Gln Ala Ala Ser Phe Thr Glu Ala Pro Thr Leu Leu Arg Ala 375 Glu Leu Pro Gly Ala Leu Glu Ala Val Lys Lys Ala Pro Leu Gln Phe Glu Asn Ala Gly Gln Glu Thr Arg Gln His Trp Ala Thr Ser Ala Asp Gly Thr Lys Ile Pro Tyr Phe Ile Thr Gly Ala Phe Glu Glu Glu Pro Gln Asn Thr Leu Val His Ala Tyr Gly Gly Phe Glu Val Ser Leu Thr Pro Ser His Ser Pro Thr Arg Gly Ile Ala Trp Leu Glu Lys Gly Tyr Tyr Phe Val Glu Ala Asn Leu Arg Gly Gly Glu Phe Gly Pro Glu Trp His Ser Gln Ala Thr Lys Leu Asn Arg Met Lys Val Trp Glu Asp His Arg Ala Val Leu Ala Asp Leu Val Glu Arg Gly Tyr Ala Thr Pro 505 Glu Gln Ile Ala Ile Arg Gly Gly Ser Asn Gly Gly Leu Leu Thr Ser 520 525 Gly Ala Leu Thr Gln Tyr Pro Glu Ala Phe Gly Ala Ala Val Val Gln

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Thr Gln Leu Phe Leu Asp Thr Leu Ser Glu Val Glu Glu Pro Glu Val
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432

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Ser Trp Leu Gly Pro Pro Lys Ser Asn Glu Leu Thr Asn Pro Asp Gly 65 70 75 80

Val Gly Lys Arg Ser Glu Phe Phe Gly Gly Ala Ile Tyr Trp His Pro 85 90 95

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Thr Leu Asn Trp Glu Ser Gly Pro Leu Gly Tyr Pro Thr Ser Gly Pro 115 120 125

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Lys Gln Arg Tyr Glu Glu Leu Gly Gly Ser Asn His Ala Ile Gly Ile 165 170 175

Pro Ile Thr Asn Glu Leu Pro Ser Gly Thr Glu Tyr Phe Tyr Asn Asn 180 185 190

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Leu Phe His Val Ala 245

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tcg Ser	ggt Gly	gct Ala	tcc Ser 25	act Thr	acc Thr	tct Ser	acc Thr	tct Ser 30	tct Ser	tat Tyr	gag Glu	gct Ala	aag Lys 35	cag Gln	gta Val	211
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gtt Val	att Ile 55	tct Ser	ttt Phe	ctg Leu	cct Pro	gag Glu 60	gtt Val	gtg Val	gga Gly	gaa Glu	gtc Val 65	cgt Arg	aag Lys	gtt Val	att Ile	307
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ttc Phe	ttg Leu	att Ile	gtt Val	ttg Leu 90	acc Thr	gct Ala	ttg Leu	gtg Val	tct Ser 95	ggt Gly	gtg Val	gat Asp	ttc Phe	cta Leu 100	gct Ala	403
ggt Gly	ctt Leu	gga Gly	gtt Val 105	gag Glu	aag Lys	att Ile	ctg Leu	act Thr 110	ccg Pro	tago	gtago	gat o	gtgta	acat	C	453
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Val 65	Arg	Lys	Val	Ile	Trp 70	Pro	Thr	Ala	Arg	Gln 75	Met	Val	Thr	Tyr	Thr 80	
Leu	Val	Val	Leu	Gly 85	Phe	Leu	Ile	Val	Leu 90	Thr	Ala	Leu	Val	Ser 95	Gly	
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gac aac ctc gca gag ttc aac ctc gtc aac acc gaa ctg ggc gag Asp Asn Leu Ala Glu Phe Asn Leu Val Asn Thr Glu Leu Gly Glu 25 30 35	gtc 211 Val
tcc tca aag gac ttc cag ggc cgc aag ctt gtc ctg aac atc ttc Ser Ser Lys Asp Phe Gln Gly Arg Lys Leu Val Leu Asn Ile Phe 40 45 50	cca 259 Pro
tcc gtt gac acc ggc gtt tgt gca aca tca gtc cgc aag ttc aac Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val Arg Lys Phe Asn 55 60 65	gag 307 Glu
gca gca gca agc ctg gaa aac acc acc gtg ctg tgc atc tcc aag Ala Ala Ala Ser Leu Glu Asn Thr Thr Val Leu Cys Ile Ser Lys 70 75 80	gat 355 Asp 85
ctt cca ttc gca ctg ggc cgt ttc tgc tcc gca gaa ggc atc gag a Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala Glu Gly Ile Glu 290 95 100	aac 403 Asn
gtc acc cca gta tcc gca ttc cgt tcc acc ttc ggt gaa gac aac (Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe Gly Glu Asp Asn (105)	ggc 451 Gly
atc gtg ctc gaa ggc tca cca ctt aag ggt ctt ctt gca cgc agc c Ile Val Leu Glu Gly Ser Pro Leu Lys Gly Leu Leu Ala Arg Ser v 120 125 130	gtc 499 Val
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gag atc ttc act gaa cct gat tac gac gct gca ctt gct ggg ctg a Glu Ile Phe Thr Glu Pro Asp Tyr Asp Ala Ala Leu Ala Gly Leu A 150 155 160	aac 595 Asn 165
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Glu Leu Gly Glu Val Ser Ser Lys Asp Phe Gln Gly Arg Lys Leu Val 35 40 45

Leu Asn Ile Phe Pro Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val 50 55 60

Arg Lys Phe Asn Glu Ala Ala Ala Ser Leu Glu Asn Thr Thr Val Leu 65 70 75 80

Cys Ile Ser Lys Asp Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala 85 90 95

Glu Gly Ile Glu Asn Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe 100 105 110

Gly Glu Asp Asn Gly Ile Val Leu Glu Gly Ser Pro Leu Lys Gly Leu 115 120 125

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Met Ile Leu His Gly

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ctg Leu 70	GIN	tct Ser	aag Lys	gcc Ala	act Thr 75	gtg Val	acc Thr	tca Ser	ggt Gly	cta Leu 80	gga Gly	aag Lys	agc Ser	ttt Phe	tta Leu 85	355
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Gly Phe Val Gln Ile Phe Gly Gly Gly Phe Asp Phe Gly Lys Ala Leu 50 55 60

Pro Gly Leu Asp Arg Leu Gln Ser Lys Ala Thr Val Thr Ser Gly Leu 65 70 75 80

Gly Lys Ser Phe Leu Leu Gly Met Thr Ser Ser Ile Ala Gly Phe Cys 85 90 95

Ser Gly Pro Ile Leu Gly Ala Val Leu Thr Leu Ala Ala Thr Ser Gly 100 105 110

Asn Ser Ile Thr Ser Ala Leu Ile Leu Ser Ala Tyr Gly Ala Gly Met 115 120 125

Val Leu Pro Leu Met Ala Ile Ala Ala Leu Trp Ala Lys Leu Gly Gln 130 135 140

Arg Gly Gln Gln Met Leu Arg Gly Arg Glu Phe Thr Phe Leu Gly Arg 145 150 155 160

Gln Trp His Ile Val Ser Val Ile Ser Gly Ala Leu Ile Ile Ala Val 165 \$170\$

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Val Pro Met Asp Thr Gln Ile Trp Leu Gln Glu Ala Thr Phe Ser Leu 195 200 205

Gly Ser Pro Leu Phe Asp Ile Ala Leu Ile Ile Val Ala Ala Gly Leu 210 215 220

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Phe Glu Asn Gln Val Val Ile Leu Asn Ala Trp Gly Gln Trp Cys Ala
Pro Cys Arg Ser Glu Ser Asp Asp Leu Gln Ile Ile His Glu Glu Leu
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Asn Gly Leu Asp Tyr Pro Ser Ile Tyr Asp Pro Pro Phe Met Thr Ala
Ala Ser Leu Gly Gly Val Pro Ala Ser Val Ile Pro Thr Thr Ile Val
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883

931

977

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Pro	His	Glu 35	Gly	Lys	Val	Ala	Asn 40	Ile	Thr	Lys	Val	Thr 45	Ser	Ser	Asn
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Gln	Ile	Pro 115	Val	Ala	Tyr	Val	Val 120	Lys	Asp	Gly	Ala	Ser 125	Ile	Ala	Glu
Phe	Asn 130	Ser	Leu	Asn	Lys	Glu 135	Pro	Val	Ala	Gln	Trp 140	Leu	Asp	His	Phe
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Thr	Val	Lys	Arg	Ala	His	Ala	Ala	Val	Ser	Val	Leu	Ala	Arg	Met	Ser

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95

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Ile Asn Leu Asn Glu Ala Gly Glu Glu Val Phe Gly Thr Ala Arg Arg

Ile Thr Val Ser Lys Asp Glu Thr Ile Ile Val Asp Gly Ala Gly Ser

330

Ala Glu Asp Val Glu Ala Arg Arg Gly Gln Ile Arg Arg Glu Ile Ala 340 345 350

Asn Thr Asp Ser Thr Trp Asp Arg Glu Lys Ala Glu Glu Arg Leu Ala 355 360 365

Lys Leu Ser Gly Gly Ile Ala Val Ile Arg Val Gly Ala Ala Thr Glu 370 380

Thr Glu Val Asn Asp Arg Lys Leu Arg Val Glu Asp Ala Ile Asn Ala 385 390 395 400

Ala Arg Ala Ala Gln Glu Gly Val Ile Ala Gly Gly Gly Ser Ala
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Leu Val Gln Ile Ala Glu Thr Leu Lys Ala Tyr Ala Glu Glu Phe Glu 420 425 430

Gly Asp Gln Lys Val Gly Val Arg Ala Leu Ala Thr Ala Leu Gly Lys
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Val Ala Arg Thr Ala Ala Leu Pro Asn Gly Glu Gly Phe Asn Ala Ala 465 470 475 480

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Thr Phe Asp Ile Asp Ala Asn Gly Ile Val His Val Thr Ala Lys Asp

450

460

455

Lys Gly Thr Gly Lys Glu Asn Thr Ile Thr Ile Gln Asp Gly Ser Gly 475 Leu Ser Gln Asp Glu Ile Asp Arg Met Ile Lys Asp Ala Glu Ala His 485 Ala Asp Glu Asp Lys Lys Arg Arg Glu Glu Glu Val Arg Asn Asn 505 Ala Glu Ser Leu Val Tyr Gln Thr Arg Lys Phe Val Glu Glu Asn Ser 515 Glu Lys Val Ser Glu Asp Leu Lys Ala Lys Val Glu Glu Ala Ala Lys 535 Gly Val Glu Glu Ala Leu Lys Gly Glu Asp Leu Glu Ala Ile Lys Ala 545 Ala Val Glu Lys Leu Asn Thr Glu Ser Gln Glu Met Gly Lys Ala Ile Tyr Glu Ala Asp Ala Ala Gly Ala Thr Gln Ala Asp Ala Gly Ala 580 585 Glu Gly Ala Ala Asp Asp Asn Val Val Asp Ala Glu Val Val Glu Asp Asp Ala Ala Asp Asn Gly Glu Asp Lys Lys 610 615 <210> 601 <211> 1575 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1552) <223> RXN01345 <400> 601 cataacctca ttgaacatgc aaaactaatg cttttggggg gtatgcataa attcgtttcg 60 ttccactgca cagcccgaaa atgctgctag ggtcaagttc atg cgt ttt gga ctt 115 Met Arg Phe Gly Leu gac ttg gga act acc cgc aca atc gcg gcc gcc gtg gac cgc gga aac 163 Asp Leu Gly Thr Thr Arg Thr Ile Ala Ala Ala Val Asp Arg Gly Asn tat ccc atc gtc act gtg gaa gat tct tta ggc gac acc cac gat ttc 211 Tyr Pro Ile Val Thr Val Glu Asp Ser Leu Gly Asp Thr His Asp Phe att cca tct gtg gtg gcc ctc aag gca gat agg att gtc gcg ggt tgg 259 Ile Pro Ser Val Val Ala Leu Lys Ala Asp Arg Ile Val Ala Gly Trp 45

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Ile Val Ala Gly Trp Asp Ala Ile Glu Val Gly Gln Asp His Pro Ser 50 55 60

Phe Val Arg Ser Phe Lys Arg Leu Leu Ser Glu Pro Asn Val Thr Glu 65 70 75 80

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Thr Gln Leu Gly Asp Thr Ser Pro Ile Glu Val Val Ile Gly Val Pro 115 120 125

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Ala Thr Gly Ile Thr Val Val Gly Leu Val Asn Glu Pro Ser Ala Ala 145 150 155 160

Ala Phe Glu Tyr Thr His Arg His Ala Arg Thr Leu Asn Ser Lys Arg 165 170 175

Gln Ala Ile Val Val Tyr Asp Leu Gly Gly Gly Thr Phe Asp Ser Ser 180 185 190

Leu Ile Arg Ile Asp Gly Thr His His Glu Val Val Ser Ser Ile Gly 195 200 205

Ile Ser Arg Leu Gly Gly Asp Asp Phe Asp Glu Ile Leu Leu Gln Cys 210 215 220

Ala Leu Lys Ala Ala Gly Arg Gln His Asp Ala Phe Gly Lys Arg Ala 225 230 235 240

Lys Asn Thr Leu Leu Asp Glu Ser Arg Asn Ala Lys Glu Ala Leu Val 245 250 255

Pro Gln Ser Arg Arg Leu Val Leu Glu Ile Gly Asp Asp Asp Ile Thr 260 265 270

Val Pro Val Asn Lys Phe Tyr Glu Ala Ala Thr Pro Leu Val Glu Lys 275 280 285

Ser Leu Ser Ile Met Glu Pro Leu Ile Gly Val Asp Asp Leu Lys Asp 290 295 300

Ser Asp Ile Ala Gly Ile Tyr Leu Val Gly Gly Gly Ser Ser Leu Pro 305 310 315

Leu Val Ser Arg Leu Leu Arg Glu Arg Phe Gly Arg Arg Val His Arg 325 330 335

Ser Pro Phe Pro Ser Gly Ser Thr Ala Val Gly Leu Ala Ile Ala Ala 340 345 350

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gat Asp 70	aaa Lys	act Thr	gca Ala	gaa Glu	aac Asn 75	Lys	gtt Val	gac Asp	gca Ala	gaa Glu 80	gtc Val	cgt Arg	atc Ile	ggt Gly	ggc Gly 85	355
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gag Glu	ctt Leu 295	cgc Arg	cac His	atg Met	gat Asp	cca Pro 300	gat Asp	ttg Leu	ggc Gly	tac Tyr	cag Gln 305	cac His	gca Ala	cta Leu	tcc Ser	1027

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1080

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1010) COLYMODACCELLUM GIUCAMICUM

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Thr Glu Ser Thr Asn Glu Ala Ser Arg Glu His Pro Ser Arg Val Ile 50 55 60

Ile Leu Val Val Gly Asp Lys Thr Ala Glu Asn Lys Val Asp Ala Glu 65 70 75 80

Val Arg Ile Gly Gly Asp Ala Gly Ala Ser Glu Met Ile Ile Met His
85 90 95

Leu Asn Gly Pro Val Ala Asp Lys Leu Gln Tyr Val Val Thr Pro Leu 100 105 110

Leu Leu Pro Asp Thr Pro Ile Val Ala Trp Trp Pro Gly Glu Ser Pro 115 120 125

Lys Asn Pro Ser Gln Asp Pro Ile Gly Arg Ile Ala Gln Arg Arg Ile 130 135 140

Thr Asp Ala Leu Tyr Asp Arg Asp Asp Ala Leu Glu Asp Arg Val Glu 145 150 155 160

Asn Tyr His Pro Gly Asp Thr Asp Met Thr Trp Ala Arg Leu Thr Gln 165 170 175

Trp Arg Gly Leu Val Ala Ser Ser Leu Asp His Pro Pro His Ser Glu 180 185 190

Ile Thr Ser Val Arg Leu Thr Gly Ala Ser Gly Ser Thr Ser Val Asp 195 200 205

Leu Ala Ala Gly Trp Leu Ala Arg Arg Leu Lys Val Pro Val Ile Arg 210 215 220

Glu Val Thr Asp Ala Pro Thr Val Pro Thr Asp Glu Phe Gly Thr Pro 225 230 235 240

Leu Leu Ala Ile Gln Arg Leu Glu Ile Val Arg Thr Thr Gly Ser Ile 245 250 255

Ile Ile Thr Ile Tyr Asp Ala His Thr Leu Gln Val Glu Met Pro Glu 265 Ser Gly Asn Ala Pro Ser Leu Val Ala Ile Gly Arg Arg Ser Glu Ser 275 Asp Cys Leu Ser Glu Glu Leu Arg His Met Asp Pro Asp Leu Gly Tyr Gln His Ala Leu Ser Gly Leu Ser Ser Val Lys Leu Glu Thr Val 310 315 <210> 605 <211> 1947 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1924) <223> RXN02280 <400> 605 egegattgeg teategateg ttgttgette catgegeace acaetatett tetgeaegee 60 ctgatgccct gtggattcaa aactgtgctt ttataggcgt atg caa gaa tcc tca 115 Met Gln Glu Ser Ser 163 cgt gat aat ttc caa gtt gac ctc ggc ggc gtt gtt gat ctt ttg agt Arg Asp Asn Phe Gln Val Asp Leu Gly Gly Val Val Asp Leu Ser 10 211 cgc cac att tat tcc ggt ccg agg gtg tat gtg cgt gag ttg ctg cag Arg His Ile Tyr Ser Gly Pro Arg Val Tyr Val Arg Glu Leu Leu Gln 2.5 aat gcg gtt gat gct tgt act gca cgt tct gaa cag ggt gag gag ggc 259 Asn Ala Val Asp Ala Cys Thr Ala Arg Ser Glu Gln Gly Glu Glu Gly 40 307 tac gag ccg agt att cgt att cgg ccg gtg acc aag gat cgt gcc acg Tyr Glu Pro Ser Ile Arg Ile Arg Pro Val Thr Lys Asp Arg Ala Thr ttt tca ctg gtt gat aat ggt acg ggc ctg acc gcg cag gag gcg cgg 355 Phe Ser Leu Val Asp Asn Gly Thr Gly Leu Thr Ala Gln Glu Ala Arg gaa ttg ctg gcg acg gtg ggg cgg acg tcg aaa cgc gat gaa ttc ggt 403 Glu Leu Leu Ala Thr Val Gly Arg Thr Ser Lys Arg Asp Glu Phe Gly ctg cag cgg gaa ggt cgc ctg ggg caa ttt ggc atc ggg ctg ctt agt 451 Leu Gln Arg Glu Gly Arg Leu Gly Gln Phe Gly Ile Gly Leu Leu Ser 110 tgt ttc atg gtg gcg gat gag atc acc atg gtg tcg cat gcg gag ggt 499 Cys Phe Met Val Ala Asp Glu Ile Thr Met Val Ser His Ala Glu Gly 120 125

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gag Glu 150	att Ile	ctt Leu	ggg	gat Asp	gac Asp 155	gca Ala	acg Thr	gat Asp	gtc Val	att Ile 160	ccg Pro	gtg Val	ggc	acg Thr	act Thr 165	595
gtg Val	cac His	ctg Leu	act Thr	ccg Pro 170	cgc Arg	cct Pro	gat Asp	gag Glu	cgc Arg 175	acg Thr	ttg Leu	ctg Leu	acg Thr	gaa Glu 180	aat Asn	643
tcc Ser	gtg Val	gtc Val	acc Thr 185	att Ile	gct Ala	agt Ser	aat Asn	tat Tyr 190	ggc Gly	cgc Arg	tac Tyr	ctg Leu	ccg Pro 195	att Ile	cct Pro	691
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tcg Ser	tgg Trp	ctg Leu	att Ile	aat Asn 330	ctc Leu	gcc Ala	atg Met	acc Thr	aag Lys 335	cct Pro	cac His	cgc Arg	gtg Val	cgg Arg 340	gaa Glu	1123
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gcg Ala	gac Asp	ctg Leu 360	gct Ala	gaa Glu	acc Thr	atg Met	ttg Leu 365	ggt Gly	ctt Leu	ctc Leu	acc Thr	ttg Leu 370	gag Glu	acc Thr	tcc Ser	1219

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	cgt Arg	ggt Gly 375	cgc Arg	atc Ile	tcg Ser	atc Ile	ggt Gly 380	gag Glu	atc Ile	acc Thr	acg Thr	ttg Leu 385	tcc Ser	atc Ile	acc Thr	gag Glu	1267
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E	ccg Pro	ccg Pro 455	ctg Leu	cag Gln	gac Asp	att Ile	gag Glu 460	aaa Lys	gcc Ala	aag Lys	gca Ala	ctg Leu 465	gat Asp	gcg Ala	cag Gln	gtc Val	1507
1	acg Thr 170	gaa Glu	tca Ser	ttg Leu	aag Lys	gat Asp 475	ttt Phe	cag Gln	atc Ile	aag Lys	ggc Gly 480	gca Ala	acg Thr	agg Arg	gtt Val	ttt Phe 485	1555
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P	gcc Ala	tca Ser	cgg Arg	gat Asp 505	cgc Arg	aat Asn	gaa Glu	aca Thr	caa Gln 510	agc Ser	gca Ala	acc Thr	act Thr	gat Asp 515	cgt Arg	tgg Trp	1651
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9 A	at .sp	ctg Leu	gtt Val 600	tct Ser	ttg Leu	tct Ser	ttg Leu	tca Ser 605	tcc Ser	gat Asp	atc Ile	taag	jacaa	itc c	tecç	gctaat	1944
С	tt																1947

ctt

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Gln Gly Glu Gly Tyr Glu Pro Ser Ile Arg Ile Arg Pro Val Thr 50 55 60

Lys Asp Arg Ala Thr Phe Ser Leu Val Asp Asn Gly Thr Gly Leu Thr 65 70 75 80

Ala Gln Glu Ala Arg Glu Leu Leu Ala Thr Val Gly Arg Thr Ser Lys 85 90 95

Arg Asp Glu Phe Gly Leu Gln Arg Glu Gly Arg Leu Gly Gln Phe Gly 100 105 110

Ile Gly Leu Leu Ser Cys Phe Met Val Ala Asp Glu Ile Thr Met Val 115 120 125

Ser His Ala Glu Gly Ala Ser Ala Ile Arg Trp Thr Gly His Ala Asp 130 135 140

Gly Thr Phe Asn Leu Glu Ile Leu Gly Asp Asp Ala Thr Asp Val Ile 145 150 155 160

Pro Val Gly Thr Thr Val His Leu Thr Pro Arg Pro Asp Glu Arg Thr 165 170 175

Leu Leu Thr Glu Asn Ser Val Val Thr Ile Ala Ser Asn Tyr Gly Arg 180 185 190

Tyr Leu Pro Ile Pro Ile Val Val Gln Gly Glu Lys Asn Thr Thr Ile 195 200 205

Thr Thr Ser Pro Val Phe Ala Lys Asp Thr Asp Gln Gln His Arg Leu 210 215 220

Tyr Ala Gly Arg Glu Arg Leu Gly Lys Thr Pro Phe Asp Val Ile Asp 225 230 235 240

Leu Thr Gly Pro Gly Ile Glu Gly Val Ala Tyr Val Leu Pro Glu Ala 245 250 255

Gln Ala Pro His Met Ser Arg Arg His Ser Ile Tyr Val Asn Arg Met $260 \\ \hspace{1.5cm} 265 \\ \hspace{1.5cm} 270 \\ \hspace{1.5cm}$

Leu Val Ser Asp Gly Pro Ser Thr Val Leu Pro Asn Trp Ala Phe Phe 275 280 285

Val Glu Cys Glu Ile Asn Ser Thr Asp Leu Glu Pro Thr Ala Ser Arg 290 295 300 Glu Ala Leu Met Asp Asp Thr Ala Phe Ala Ala Thr Arg Glu His Ile 310 315 Gly Glu Cys Ile Lys Ser Trp Leu Ile Asn Leu Ala Met Thr Lys Pro 330 335 His Arg Val Arg Glu Phe Thr Ala Ile His Asp Leu Ala Leu Arg Glu Leu Cys Gln Ser Asp Ala Asp Leu Ala Glu Thr Met Leu Gly Leu Leu Thr Leu Glu Thr Ser Arg Gly Arg Ile Ser Ile Gly Glu Ile Thr Thr Leu Ser Ile Thr Glu Asp Val Ser Leu Gln Leu Ala Thr Thr Leu Asp Asp Phe Arg Gln Leu Asn Thr Ile Ala Arg Pro Asp Thr Leu Ile Ile 410 Asn Gly Gly Tyr Ile His Asp Ser Asp Leu Ala Arg Leu Ile Pro Val His Tyr Pro Pro Leu Thr Val Ser Thr Ala Asp Leu Arg Glu Ser Met Asp Leu Met Glu Leu Pro Pro Leu Gln Asp Ile Glu Lys Ala Lys Ala 455 Leu Asp Ala Gln Val Thr Glu Ser Leu Lys Asp Phe Gln Ile Lys Gly Ala Thr Arg Val Phe Glu Pro Ala Asp Val Pro Ala Val Ile Ile Asp Ser Lys Ala Gln Ala Ser Arg Asp Arg Asn Glu Thr Gln Ser Ala Thr Thr Asp Arg Trp Ala Asp Ile Leu Ala Thr Val Asp Asn Thr Leu 520 Ser Arg Gln Thr Ala Asn Ile Pro Gln Asp Gln Gly Leu Ser Ala Leu Cys Leu Asn Trp Asn Asn Ser Leu Val Arg Lys Leu Ala Ser Thr Asp Asp Thr Ala Val Val Ser Arg Thr Val Arg Leu Leu Tyr Val Gln Ala Leu Leu Ser Ser Lys Arg Pro Leu Arg Val Lys Glu Arg Ala Leu Leu Asn Asp Ser Leu Ala Asp Leu Val Ser Leu Ser Leu Ser Ser Asp Ile

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ggg gtt gc Gly Val Al										163
ctt gta aa Leu Val Ly			Glu Gl							211
tat gtt cc Tyr Val Pr 4	o Asn Arg									259
ttc gaa tc Phe Glu Se 55										307
aac gat ag Asn Asp Se 70	t aaa gac r Lys Asp	aat gtt Asn Val 75	gag ga Glu Gl	aa ctt Lu Leu	ccg c Pro I 80	cta cct Leu Pro	aag c Lys A	Arg A	ac sp 85	355
atc gtt gc Ile Val Al							Pro G			403
gtg agc aa Val Ser Ly				al Glu						451
aat gag gg Asn Glu Gl 12	y Ala Arg									499
cca aca gg Pro Thr Gl 135					Leu A					547
gtt gga gg Val Gly Gl 150				ly Pro				Glu L		595

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ato Ile	: tat : Tyr	tgg Trp	cat His 185	cca Pro	gac Asp	aca Thr	ggc Gly	gct Ala 190	tat Tyr	gca Ala	gtg Val	acc Thr	ctg Leu 195	gac Asp	ggt Gly	691
ttg Leu	agg Arg	cag Gln 200	tgg Trp	Gly	acc Thr	ttg Leu	aac Asn 205	tgg Trp	gaa Glu	tca Ser	ggg	cca Pro 210	ttg Leu	GJA aaa	tac Tyr	739
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Pro	Asp	Asp	Glu	Glu 410	Arg	Ser	Leu	Glu	Asp 415	Phe	Leu	Pro	Ile	Gly 420	Ser	
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					tgc Cys											1459
aaa Lys	act Thr 455	gaa Glu	aac Asn	aac Asn	att Ile	gaa Glu 460	aag Lys	aat Asn	ggt Gly	ggc Gly	ccg Pro 465	atc Ile	aaa Lys	aaa Lys	gag Glu	1507
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					tac Tyr											1603
					ttc Phe											1651
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		ctt Leu			tgac	agaa	icc (ccato	caact	g tọ	jc					1977
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Leu Pro Lys Arg Asp Ile Val Ala Gly Glu Met Arg Ser Asp Val Ile Glu Leu Pro Glu Gly Val Ser Lys Asp Glu Ala Asp Gln Val Glu Val Ala Glu Ala Arg Leu Asn Glu Gly Ala Arg Leu Met Ala Ala Thr Gly Cys Glu Ala Met Trp Pro Thr Gly Phe Ser Val Cys Gly Arg Ile Leu Asp Ala Tyr Arg Gln Val Gly Gly Gln Leu Ser Trp Leu Gly Pro Pro Lys Ser Asn Glu Leu Thr Asn Pro Asp Gly Val Gly Lys Arg Ser Glu 170 Phe Val Gly Gly Ala Ile Tyr Trp His Pro Asp Thr Gly Ala Tyr Ala 185 Val Thr Leu Asp Gly Leu Arg Gln Trp Gly Thr Leu Asn Trp Glu Ser 205 Gly Pro Leu Gly Tyr Pro Thr Ser Gly Pro Met Asp Thr Asn Tyr Pro Leu Thr Gln Arg Gln Thr Phe Gln Gly Gly Asp Asn Tyr Tyr Asn Pro 235 Leu Thr Gly Gly Ala Val Trp Gly Asp Ile Lys Gln Arg Tyr Glu Glu Leu Gly Gly Ser Asn His Ala Ile Gly Ile Pro Ile Thr Asn Glu Leu Pro Ser Gly Thr Glu Tyr Phe Tyr Asn Asn Phe Phe Asn Gly Thr Ile 280 Ser Trp Arg Asn Asp Arg Gln Thr Arg Phe Met Tyr Leu Ala Thr Gln 295

Arg Val Trp Asp Ala Leu Gly Arg Glu Thr Gly Arg Leu Gly Phe Pro 305 310 315 320

Glu Ala Asp Glu Thr Pro Glu Val Ser Gly Leu Phe His Val Val Asn 325 Phe Ala Glu Arg Gly Val Ile Ala Trp Asn Gly Ile Leu Gly Ala Arg 345 340 Glu Leu Tyr Gly Asp Val Tyr Ser Leu Trp Leu Gln Tyr Gln Asn Thr 360 Asp Thr Pro Leu Gly Trp Pro Ile Pro Ser Leu Thr Ser Leu Asn Glu 375 Ser Leu Glu Gln Glu Phe Thr Arg Gly Val Val Leu Gly Ser Gly Asp Ala Leu Thr Trp Ile Pro Asp Asp Glu Glu Arg Ser Leu Glu Asp Phe Leu Pro Ile Gly Ser Ser Gly Ser Ser Ser Ser Gln Glu Met Thr 425 Leu Phe Ser Gln Arg Ala Gln Tyr Val Asp Cys Lys Asn Leu Pro Asp Leu Asp Glu Gln Arg Lys Thr Glu Asn Asn Ile Glu Lys Asn Gly Gly Pro Ile Lys Lys Glu Tyr Ser Ser Arg Gly Phe Pro Thr Glu Phe Arg 475 Phe Val Val Arg Lys Gly His Tyr Asp Arg Tyr Arg Asn Glu Gly Trp 490 Gly Tyr Leu Lys Asn Tyr Cys Lys His Asn Phe Ala Asn His Ala Met 505 510 Ala Glu Ala Val Val Asp Lys Ala Val Ile Asp Tyr Gly Ser Ser Pro Gly Thr Ser Tyr Tyr Lys Phe Glu Lys Thr Val Tyr Phe Leu Asp Cys Arg Thr Tyr Thr Phe Asn Lys Asn Ser Gly Cys Lys Glu Met His Ala 555 Pro Gln Trp Val Thr Ile Ile Tyr Asn Pro His Thr Phe Thr Gly Ala 570 575 Asn Ser Asn Arg Pro Lys Gly Val Ile Ser Ala Trp Cys Asn Ser Thr

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605

His Val Asn Leu Tyr Asn Lys Leu Arg Ile 610 615

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ttg acc gcc Leu Thr Ala				Sly L							163
tac ctc aat Tyr Leu Asn											211
gac agt gaa Asp Ser Glu 40											259
gca gtc acc Ala Val Thr 55	gcc cag Ala Gln	ggt gaa Gly Glu 60	ggc g Gly G	gga g Gly G	gc gct ly Ala	cgc Arg 65	acc Thr	gtc Val	aag Lys	gaa Glu	307
ttc cag cgt Phe Gln Arg 70											355
aaa aaa gac Lys Lys Asp				Arg A							403
tgg tca cag Trp Ser Gln			Glu I				-				451
acc aac gga Thr Asn Gly 120											499
gtt tcc acc Val Ser Thr 135											547
gat gaa aac Asp Glu Asn 150	Gly Gln	-		-		-	-		_		595
cca gca gca Pro Ala Ala	_	_	-	Glu A	-	-		_	_		643
gca cct gtc Ala Pro Val		-	Pro A					_	-		691

-	-	-			-		gac Asp 205			_		_				739
				_		-	gcc Ala	-	-	-	-				-	787
_			-			-	gat Asp	-					-		-	835
_	_		_		-		aag Lys				-	-				883
		-	_	_	_	-	tca Ser					-	_		_	931
							act Thr 285	_								979
	_	-	_	-	_	_	cgt Arg	_	-		-			_	_	1027
					_		gga Gly		_		_	_		_		1075
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	_		-				aac Asn	_				_			-	1171
							gct Ala 365									1219
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							ggc Gly									1411

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aa As	ac aca sn Thr 455	Gly	ggc Gly	acg Thr	act Thr	acc Thr 460	acc Thr	ccg Pro	gcg Ala	aca Thr	acg Thr 465	ccg Pro	aag Lys	gag Glu	acg Thr	1507
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gc Al	t gcc a Ala	act Thr 600	ggt Gly	ggc Gly	gaa Glu	acc Thr	acc Thr 605	gtg Val	aag Lys	tac Tyr	acc Thr	agc Ser 610	gac Asp	cag Gln	aac Asn	1939
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ga Gl	a tac u Tyr	acc Thr	gtt Val 665	ggc Gly	gaa Glu	cag Gln	ctt Leu	cgt Arg 670	gtt Val	gat Asp	ttc Phe	cag Gln	aat Asn 675	ggt Gly	tac Tyr	2131
at	c act	tac	gat	tct	gcg	act	ggc	cag	gca	agc	att	cag	ctg	aac		2176

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2199

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<212> PRT

<213> Corynebacterium glutamicum

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Val Val Glu Asp Ala Ala Val Thr Ala Gln Gly Glu Gly Gly Gly Ala 50

Arg Thr Val Lys Glu Phe Gln Arg Asp Gln Gln Phe Ser Ser Phe Ala

Leu Thr Trp Thr Gly Lys Lys Asp Ile Thr Ala Phe Val Arg Ala Glu

Gln Glu Asp Gly Thr Trp Ser Gln Trp Tyr Asp Leu Glu Pro Met Val

Asn Glu Asp Gln Gly Thr Asn Gly Thr Glu Leu Ile Trp His Gly Pro 120

Thr Asn Lys Ile Gln Val Ser Thr Leu Asn Val Asp Leu Phe Gly Ala 135

Asp Ala Ala Ala Asp Glu Asn Gly Gln Asp Ile Pro Ala Val Asp 145 155

Ala Ala Glu Ala Ala Pro Ala Ala Glu Pro Ala Pro Ala Glu Ala Pro

Val Glu Glu Ala Pro Ala Pro Val Ala Glu Pro Ala Pro Ala Ala Glu 185

Pro Ile Ala Glu Pro Val Ala Asp Tyr Ser Ala Asn Asp Gly Leu Ala

Pro Leu Pro Ser Asn Tyr Gly Asp Ile Gln Pro Val Ala Asp Val Asp 210

Asp Gly Leu Asn Ala Val Phe Ile Asp Gly Asn Ala Asp Ala Gly Val 230

Gly Ile Ala Asn Val Ala Asp Thr Asp Gly Met Pro Lys Val Ile Ser

Arg Ala Gly Trp Gly Ala Asp Glu Ser Leu Arg Cys Ser Asn Pro Thr

260 265 Ile Asp Asp Gly Val Ser Ala Ile Thr Ile His His Thr Ala Gly Ser 280 Asn Asn Tyr Thr Glu Ala Gln Ala Ala Gln Val Arg Ser Ala Tyr 295 Ser Tyr His Ala Lys Asn Leu Gly Trp Cys Asp Ile Gly Tyr Gln Ser 310 315 Leu Val Asp Lys Tyr Gly Asn Ile Tyr Glu Gly Arg Ala Gly Gly Met 330 335 Thr Asn Ala Val Gln Gly Ala His Ala Gly Gly Phe Asn Gln Asn Thr Trp Ala Ile Ser Met Ile Gly Asp Tyr Ser Tyr Asn Ala Pro Pro Gln 360 Glu Thr Ile Asn Ala Val Gly Glu Leu Ala Gly Trp Arg Ala Lys Val Ala Gly Phe Asp Pro Thr Gly Thr Asp Thr His Tyr Ser Glu Gly Thr Ser Tyr Ala Lys Tyr Ser Tyr Gly Thr Arg Val Ser Leu Pro Asn Ile Leu Ala His Arg Asn Val Gly Leu Thr Ala Cys Pro Gly Asp Ala Gly Tyr Ala Gln Met Glu Asn Ile Arg Gln Ile Val Lys Ala Lys Tyr Thr Ser Leu Gln Asn Gly Asn Thr Gly Gly Thr Thr Thr Pro Ala Thr Thr Pro Lys Glu Thr Ser Thr Ser Asn Ala Pro Ser Thr Thr Ala Gln Leu Val Thr Pro Ala Glu Pro Gln Gln Tyr Ser Glu Ser Asp Ala Leu Ala Ala Leu Leu Thr Gly Gly Ser Ser Gly Gly Thr Asp Leu Leu Asn Gly Ala Asn Ser Glu Gln Leu Leu Thr Gly Leu Gly Ser Ile Ala Ala Val Leu Ile Ala Ala Ser Leu Ala Asp Gly Gly Leu Asn Gly Leu Ile Ser Asn Val Gly Ser Asn Asn Gly Val Pro Val Leu Gly Asp Ile 555 Lys Ile Thr Asp Val Ile Pro Ile Val Asp Thr Ala Ile Asn Leu Thr Gly Asp Asn Lys Tyr Ser Arg Gly Trp Asn Asp Leu Asn Asn Thr Leu 585

Gly Pro Val Leu Gly Ala Ala Thr Gly Gly Glu Thr Thr Val Lys Tyr 595 600 Thr Ser Asp Gln Asn Ser Glu Val Thr Phe Val Pro Phe Glu Asn Gly 615 Ile Met Val Ser Ser Pro Glu Ala Gly Thr His Gly Leu Trp Gly Ala Ile Gly Asp Ala Trp Ala Gln Gln Gly Ala Asp Leu Gly Pro Leu Gly Leu Pro Thr Ser Asn Glu Tyr Thr Val Gly Glu Gln Leu Arg Val Asp 660 Phe Gln Asn Gly Tyr Ile Thr Tyr Asp Ser Ala Thr Gly Gln Ala Ser 680 Ile Gln Leu Asn 690 <210> 611 <211> 702 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(679) <223> RXS02650 <400> 611 qaatttttqc tqcaactqtq taaaaaccaq cqctqaatta aagatcacct ttcaccctta 60 attgagectg ggtggaagtt tetacegete atggggaaag atg gte aac gtg acc Met Val Asn Val Thr 1 163 tca aag gat gca ggg gca aac gtg acc ccc atg agt aag aaa gaa aag Ser Lys Asp Ala Gly Ala Asn Val Thr Pro Met Ser Lys Lys Glu Lys 20 10 agg aca acc gtt aaa cag gtg gtt gcc ttg atg gcc gcc atc gtt gtg 211 Arg Thr Thr Val Lys Gln Val Val Ala Leu Met Ala Ile Val Val 35 2.5 30 gtg att gcg tcc cta gac caa ata gtc aag cag att atg ctt agt tgg 259 Val Ile Ala Ser Leu Asp Gln Ile Val Lys Gln Ile Met Leu Ser Trp 40 ttg gaa cct ggc gtt ccc gtt ccc atc att ggg gat tgg ttc cgc ttc 307 Leu Glu Pro Gly Val Pro Val Pro Ile Ile Gly Asp Trp Phe Arg Phe 55 355 tac ctc ctg ttt aac ccc gga gcc gca ttt tcg atg ggt ggg gaa aac Tyr Leu Leu Phe Asn Pro Gly Ala Ala Phe Ser Met Gly Gly Glu Asn age ace tgg ate tit aca ace ate eag ttg age tte gte ate ggt ate 403

Ser	Thr	Trp	Ile	Phe 90	Thr	Thr	Ile	Gln	Leu 95	Ser	Phe	Val	Ile	Gly 100	Ile	
	att Ile															451
	ctt Leu															499
	gat Asp 135															547
	aac Asn															595
	gtg Val															643
	cat His											tgat	gaad	caa		689
ccga	acaaa	igc a	aga													702
<210> 612 <211> 193 <212> PRT <213> Corynebacterium glutamicum																
)> 61 Val		Val	Thr 5	Ser	Lys	Asp	Ala	Gly 10	Ala	Asn	Val	Thr	Pro 15	Met	
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Ala	Ala	Ile 35	Val	Val	Val	Ile	Ala 40	Ser	Leu	Asp	Gln	Ile 45	Val	Lys	Gln	
Ile	Met 50	Leu	Ser	Trp	Leu	Glu 55	Pro	Gly	Val	Pro	Val 60	Pro	Ile	Ile	Gly	
Asp 65	Trp	Phe	Arg	Phe	Tyr 70	Leu	Leu	Phe	Asn	Pro 75	Gly	Ala	Ala	Phe	Ser 80	
Met	Gly	Gly	Glu	Asn 85	Ser	Thr	Trp	Ile	Phe 90	Thr	Thr	Ile	Gln	Leu 95	Ser	
Phe	Val	Ile	Gly 100	Ile	Ala	Ile	Tyr	Ala 105	Pro	Arg	Ile	Lys	His 110	Lys	Trp	
Ile	Ala	Ala 115	Gly	Leu	Ala	Leu	Val 120	Ala	Gly	Gly	Ala	Leu 125	Gly	Asn	Val	
Leu	Asp	Arg	Leu	Phe	Arg	Asp	Pro	Ser	Phe	Phe	Phe	Gly	His	Val	Val	

130 140 Asp Tyr Ile Ser Val Gly Asn Phe Ala Val Phe Asn Ile Ala Asp Ala 155 Ser Ile Ser Cys Gly Val Val Val Phe Leu Ile Gly Met Phe Leu Glu 165 170 Asp Arg Glu Asn Ala Gln His Ala Lys Ala Thr Asp Glu Lys Asp Glu 185 Ala <210> 613 <211> 1494 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1471) <223> RXS00076 <400> 613 tetaggagtg ttaaacagee tggaettgaa acacetttaa etaettgatt tteacaceet 60 tgtttccata aaagggctca cgaaaggcaa cttcaaacac atg aca act ccc ctg Met Thr Thr Pro Leu cgc gta gcc gtc atc gga gct ggc cct gct ggc att tac gca tcc gac 163 Arg Val Ala Val Ile Gly Ala Gly Pro Ala Gly Ile Tyr Ala Ser Asp 10 ctc ctc atc cgc aat gaa gag cgc gaa gtg ttc gtt gac ctt ttc gag 211 Leu Leu Ile Arg Asn Glu Glu Arg Glu Val Phe Val Asp Leu Phe Glu caa atg cct gca ccg ttc gga ctc atc cgt tac ggc gtt gct cca gac 259 Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr Gly Val Ala Pro Asp 40 cac cca cgc atc aag ggc atc gtt aag tcc ctg cac aac gtg ttg gac 307 His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu His Asn Val Leu Asp rat = 2 ± ±

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Lys 70	Pro	Arg	Leu	Arg	Leu 75	Leu	Gly	Asn	Ile	Glu 80	Ile	Gly	Lys	Asp	Ile 85	
		gaa Glu														403
		gtt Val			_	_							_	_	_	451
ggc	tcc	ttc	ggt	gcc	ggc	gag	ttc	gtt	ggc	ttc	tac	gac	ggc	aac	cca	499

Gly	Ser	Phe 120	Gly	Ala	Gly	Glu	Phe 125	Val	Gly	Phe	Tyr	Asp 130	Gly	Asn	Pro	
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					ggc Gly 155											595
ggc Gly	gac Asp	gag Glu	ctc Leu	aaa Lys 170	gtc Val	acc Thr	gaa Glu	att Ile	tcc Ser 175	gac Asp	aac Asn	gtc Val	tac Tyr	gac Asp 180	tcc Ser	643
					gcc Ala											691
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					gtg Val											787
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ggc Gly	tgg Trp	atc Ile	aag Lys	cgt Arg	gga Gly	cca Pro	atc Ile	ggt Gly	cta Leu	atc Ile	ggc Gly	aac Asn	acc Thr	aag Lys	tcc Ser	1219

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145 150 155 160 Ile Leu Ala Lys Thr Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp 170 Asn Val Tyr Asp Ser Leu Lys Glu Asn Lys Ala Thr Glu Val His Val 180 185 Phe Gly Arg Arg Gly Pro Ala Gln Val Lys Phe Thr Pro Gln Glu Leu 200 Lys Glu Leu Asp His Ser Pro Thr Ile Asn Val Val Asp Pro Glu 215 Asp Ile Asp Tyr Asp Gly Ala Ser Glu Glu Ala Arg Arg Ala Ser Lys 230 Ser Gln Asp Leu Val Cys Gln Ile Leu Glu Gln Tyr Ala Ile Arg Glu 245 Pro Lys Asp Ala Pro His Thr Leu Gln Ile His Leu Phe Glu Asn Pro 260 Val Glu Val Leu Gln Lys Asp Gly Lys Val Val Gly Leu Arg Thr Glu 280 Arg Thr Ser Leu Asp Gly Asn Gly Gly Val Asn Gly Thr Gly Glu Phe 295 Lys Asp Trp Pro Val Gln Ala Val Tyr Arg Ala Val Gly Tyr Lys Ser 305 310 Asp Pro Ile Asp Gly Val Pro Phe Asp Glu Asn Lys His Val Ile Pro Asn Asp Gly Gly His Val Leu Thr Ala Pro Gly Ala Glu Pro Val Pro 340 Gly Leu Tyr Ala Thr Gly Trp Ile Lys Arg Gly Pro Ile Gly Leu Ile Gly Asn Thr Lys Ser Asp Ala Lys Glu Thr Thr Asp Ile Leu Ile Lys 370 375 Asp Ala Val Ala Gly Val Leu Glu Ala Pro Lys His Gln Gly Glu Glu Ala Ile Ile Glu Leu Leu Asp Ser Arg Asn Ile Pro Phe Thr Trp 410 Glu Gly Trp Tyr Lys Leu Asp Ala Ala Glu Arg Ala Leu Gly Glu Ala 425 Glu Gly Arg Glu Arg Lys Lys Ile Val Asp Trp Glu Glu Met Val Arg Gln Ala Arg Glu Ala Pro Ala Ile Val

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cct Pro	ttt Phe	gac Asp	gat Asp	gag Glu 330	cgc Arg	gcg Ala	gtt Val	gtc Val	ccc Pro 335	aac Asn	gac Asp	ggc Gly	ggc Gly	cac His 340	atc Ile	1123
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gat Asp	gag Glu	cgc Arg	aag Lys	gtt Val 410	gcg Ala	ttc Phe	acc Thr	aca Thr	tgg Trp 415	gat Asp	ggc Gly	tgg Trp	cac His	ctg Leu 420	ctg Leu	1363
gat Asp	gct Ala	gcg Ala	gag Glu	cgc Arg	gcg Ala	ctg Leu	ggt Gly	gag Glu	cct Pro	gag Glu	ggc Gly	cgc Arg	gag Glu	cgc Arg	aag Lys	1411

425 430 435

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Ile Tyr Ala Ser Asp Leu Leu Met Lys Ser Asp Thr Asp Val Gln Ile 20 25 30

Asp Leu Phe Glu Arg Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr Gly 35 40 45

Val Ala Pro Asp His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu His
50 60

Asn Val Met Asp Lys Glu Gln Leu Arg Phe Leu Gly Asn Ile Glu Val 65 70 75 80

Gly Lys Asp Ile Thr Val Glu Glu Leu Arg Glu Phe Tyr Asp Ala Ile 85 90 95

Val Phe Ser Thr Gly Ala Thr Gly Asp Gln Asp Leu Arg Val Pro Gly
100 105 110 .

Ser Asp Leu Glu Gly Ser Trp Gly Ala Gly Glu Phe Val Gly Phe Tyr 115 120 125

Asp Gly Asn Pro Asn Phe Glu Arg Asn Trp Asp Leu Ser Ala Glu Lys 130 135 140

Val Ala Val Val Gly Val Gly Asn Val Ala Leu Asp Val Ala Arg Ile 145 150 155 160

Leu Ala Lys Thr Gly Asp Glu Leu Leu Val Thr Glu Ile Pro Asp Asn
165 170 175

Val Tyr Glu Ser Leu Ala Lys Asn Gln Ala Lys Glu Val His Val Phe 180 185 190

Gly Arg Gly Pro Ala Gln Ala Lys Phe Thr Pro Leu Glu Leu Lys 195 200 205

Glu Leu Asp His Ser Asp Thr Ile Glu Val Ile Val Asn Pro Glu Asp 210 215 220

Ile Asp Tyr Asp Ala Ala Ser Glu Gln Ala Arg Arg Asp Ser Lys Ser 225 230 235 240



Gln Asp Leu Val Cys Gln Thr Leu Glu Ser Tyr Ala Met Arg Asp Pro 245 250

Lys Gly Ala Pro His Lys Leu Phe Ile His Phe Phe Glu Ser Pro Val 260 265 270

Glu Ile Leu Gly Glu Asp Gly Lys Val Val Gly Leu Lys Thr Glu Arg 275 280 285

Thr Gln Leu Asp Gly Asn Gly Gly Val Thr Gly Thr Gly Glu Phe Lys 290 295 300

Thr Trp Asp Met Gln Ser Val Tyr Arg Ala Val Gly Tyr Arg Ser Asp 305 310 315

Ala Ile Glu Gly Val Pro Phe Asp Asp Glu Arg Ala Val Val Pro Asn 325 330 335

Asp Gly Gly His Ile Ile Asp Pro Glu Val Gly Ser Pro Ile Thr Gly 340 345

Leu Tyr Ala Thr Gly Trp Ile Lys Arg Gly Pro Ile Gly Leu Ile Gly 355 360 365

Asn Thr Lys Ser Asp Ala Lys Glu Thr Thr Glu Met Leu Leu Ala Asp 370 375 380

His Ala Ala Gly Ser Leu Pro Ala Pro Ala Lys Pro Glu Leu Glu Ser 385 390 395 400

Ile Ile Glu Phe Leu Asp Glu Arg Lys Val Ala Phe Thr Thr Trp Asp 405

Gly Trp His Leu Leu Asp Ala Ala Glu Arg Ala Leu Gly Glu Pro Glu 420 425 430

Gly Arg Glu Arg Lys Lys Ile Val Glu Trp Asn Asp Met Val Arg His 435 440 445

Ala Arg Pro Glu Tyr Asp Ile 450 455